

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 9, 2004, 12:21:36 ; Search time 37.3949 Seconds
(without alignments)
1795.466 Million cell updates/sec

Title: US-09-674-379A-14
Perfect score: 2407
Sequence: 1 QCTNGFDLDRQSGQCLDIDE.....INFRGSSVIRLRIYVSQYPF 423

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_19Jun03:*

- 1: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1980.DAT:*
- 2: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1981.DAT:*
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- 4: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1983.DAT:*
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- 19: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1998.DAT:*
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- 22: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA2001.DAT:*
- 23: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA2002.DAT:*
- 24: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA2003.DAT:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,

and is derived by analysis of the total score distribution.

SUMMARIES

Result		%					
No.	Score	Query	Match	Length	DB	ID	Description
1	2407	100.0	448	19	AAW79739	Human	EEGF protein
2	2407	100.0	448	20	AAW95709	Homo sapiens fetal	
3	2407	100.0	448	20	AAW94281	Human	extracellula
4	2407	100.0	448	21	AAAY57058	Amino acid sequenc	
5	2407	100.0	448	21	AAAY54989	Full length human	
6	2407	100.0	448	22	AAM93573	Human	polypeptide,
7	2407	100.0	448	23	AAU75494	Human	extracellula
8	2401	99.8	448	20	AAAY08063	Human	EGF-like hom
9	2401	99.8	448	22	AAU29227	Human	PRO polypept
10	2401	99.8	448	22	AAB31183	Amino acid sequenc	
11	2401	99.8	448	24	ABU71315	Human	PRO210 prote
12	2401	99.8	448	24	ABU72040	Novel human	secret
13	2401	99.8	448	24	ABU65772	Human	secreted/tra
14	2401	99.8	448	24	ABU66105	Novel human	secret
15	2401	99.8	448	24	ABU67141	Novel human	secret
16	2401	99.8	448	24	ABU67272	Novel human	secret
17	2401	99.8	448	24	ABU67609	Human	secreted/tra
18	2401	99.8	448	24	ABU65467	Human	PRO polypept
19	2401	99.8	448	24	ABU58603	Human	PRO polypept
20	2401	99.8	448	24	ABU56139	Human	secreted/tra
21	2401	99.8	448	24	ABU57134	Human	PRO polypept
22	2401	99.8	448	24	ABU10713	Human	secreted/tra
23	2302	95.6	423	21	AAAY56751	Smooth muscle prol	
24	2302	95.6	423	21	AAAY56753	Smooth muscle prol	
25	2302	95.6	448	21	AAAY56750	Smooth muscle prol	
26	2302	95.6	448	21	AAAY54990	Full length mouse	
27	2302	95.6	461	21	AAAY56752	Smooth muscle prol	
28	2302	95.6	461	21	AAAY54991	Full length mouse	
29	2230	92.6	392	18	AAW31705	Human	extracellula
30	1827	75.9	335	21	AAAY76008	Rat	EGF extracellu
31	1827	75.9	335	22	AAB55947	Skin cell protein,	
32	1827	75.9	335	23	ABB72147	Rat	protein isolat
33	1276.5	53.0	443	18	AAW32110	Human	extracellula
34	1276.5	53.0	443	20	AAAY16587	Extracellular prot	
35	1276.5	53.0	443	21	AAB33418	Human	PRO226 prote
36	1276.5	53.0	443	21	AAAY84707	A human	p53 mutant
37	1276.5	53.0	443	21	AAAY55850	Human	S1-5 ECMP-li
38	1276.5	53.0	443	22	AAU12330	Human	PRO226 polyp
39	1276.5	53.0	443	23	AAU86130	Human	PRO226 polyp
40	1276.5	53.0	443	24	ABU66728	Human	PRO polypept
41	1276.5	53.0	443	24	ABU67004	Human	secreted/tra
42	1276.5	53.0	443	24	ABU59809	Novel	secreted and
43	1272.5	52.9	443	21	AAAY84706	Amino acid sequenc	
44	1270.5	52.8	443	22	AAB92533	Human	protein sequ
45	1237.5	51.4	433	21	AAB58353	Lung cancer associ	

ALIGNMENTS

RESULT 1

AAW79739

ID AAW79739 standard; Protein; 448 AA.

XX

AC AAW79739;

XX

DT 25-JAN-1999 (first entry)

XX

DE Human EGF protein.

XX

KW Extracellular/epidermal growth factor-like protein; EGF; human; liver;
 KW vascular smooth muscle cell proliferation; neurology; pathology; AIDS;
 KW dementia; ocular; disorder; cornea; inflammation; tumour cell; kidney;
 KW wound; epithelium; surgery; skin graft; ulcer; diabetic; trophic;
 KW Marfan syndrome; treatment; hair follicle; embryogenesis; neoplasia;
 KW epidermal cell; cancer; psoriasis; detection.

XX

OS Homo sapiens.

XX

FH	Key	Location/Qualifiers
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FT	Peptide	1..25
----	---------	-------

FT		/label= signal
----	--	----------------

FT	Protein	26..448
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FT		/label= EGF
----	--	-------------

FT		/note= "Extracellular/epidermal growth factor-like protein"
----	--	--

FT	Region	112..153
----	--------	----------

FT		/label= EGF-1
----	--	---------------

FT	Region	154..190
----	--------	----------

FT		/label= EGF-2
----	--	---------------

FT	Region	191..230
----	--------	----------

FT		/label= EGF-3
----	--	---------------

FT	Region	231..271
----	--------	----------

FT		/label= EGF-4
----	--	---------------

FT	Region	272..314
----	--------	----------

FT		/label= EGF-5
----	--	---------------

XX

PN WO9846746-A1.

XX

PD 22-OCT-1998.

XX

PF 11-APR-1997; 97WO-US06020.

XX

PR 11-APR-1997; 97WO-US06020.

XX

PA (HUMA-) HUMAN GENOME SCI INC.

XX

PI Li H, Olsen HS;

XX

DR WPI; 1998-568728/48.

DR N-PSDB; AAV62432.

XX

PT New isolated extracellular/epidermal growth factor - used for
 PT regulating vascular smooth muscle cell proliferation, e.g. for
 PT enhancing neurological functions or treating neoplasia and other
 PT disorders.

XX

Qy 421 YPF 423
|||
Db 446 YPF 448

RESULT 2

AAW95709

ID AAW95709 standard; Protein; 448 AA.

XX

AC AAW95709;

XX

DT 21-JUN-1999 (first entry)

XX

DE Homo sapiens fetal kidney clone AK647 secreted protein.

XX

KW Secreted protein; fetal kidney.

XX

OS Homo sapiens.

XX

PN WO9900405-A1.

XX

PD 07-JAN-1999.

XX

PF 29-JUN-1998; 98WO-US13530.

XX

PR 30-JUN-1997; 97US-0885610.

XX

PA (GEMY) GENETICS INST INC.

XX

PI Agostino MJ, Evans C, Jacobs K, Lavallie ER, Mccoy JM;

PI Merberg D, Racie LA, Treacy M;

XX

DR WPI; 1999-095671/08.

DR N-PSDB; AAX07567.

XX

PT New polynucleotides encoding secreted human proteins - are derived
PT from foetal kidney or adult retina cDNA libraries, used as, e.g.
PT potential vaccines

XX

PS Claim 11; Pages 52-54; 76pp; English.

XX

CC The sequence is that of a secreted protein from a human fetal
CC kidney clone AK296. Such a sequence is predicted to have biological
CC activities which would make them suitable for treating, preventing or
CC ameliorating medical conditions in humans and animals, although no
CC supporting data is given. Suggested activities include nutritional
CC activity, cytokine and cell proliferation/differentiation activity,
CC immune stimulating (e.g. as vaccines) or suppressing activity,
CC haematopoiesis regulating activity, tissue growth activity,
CC activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic
CC and thrombolytic activity, receptor/ligand activity, anti-inflammatory
CC activity, cadherin/tumour invasion suppressor activity, and tumour
CC inhibition activity. It is also stated to be useful for gene
CC therapy.

XX

SQ Sequence 448 AA;

Query Match 100.0%; Score 2407; DB 20; Length 448;
 Best Local Similarity 100.0%; Pred. No. 1.2e-159;
 Matches 423; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	QCTNGFDLDRQSGQCLDIDECRTIPEACRGDMMCVNQNGGYLCIPRTNPVYRGPYSNPYS	60
Db	26	QCTNGFDLDRQSGQCLDIDECRTIPEACRGDMMCVNQNGGYLCIPRTNPVYRGPYSNPYS	85
Qy	61	TPYSGPYPAAAPPLSAPNYPTISRPLICRFGYQMDENQCVDVDECATDSHCNPTQICI	120
Db	86	TPYSGPYPAAAPPLSAPNYPTISRPLICRFGYQMDENQCVDVDECATDSHCNPTQICI	145
Qy	121	NTEGGYTCSC TDGYWLLEGQCLDIDECRYGYCQQLCANVPGSYSCTCNPGFTLNEDGRSC	180
Db	146	NTEGGYTCSC TDGYWLLEGQCLDIDECRYGYCQQLCANVPGSYSCTCNPGFTLNEDGRSC	205
Qy	181	QDVNECATENPCVQTCVNTYGSFICRCDPGYELEEDGVHCSDMDECSFSEFLCQHECVNQ	240
Db	206	QDVNECATENPCVQTCVNTYGSFICRCDPGYELEEDGVHCSDMDECSFSEFLCQHECVNQ	265
Qy	241	PGTYFCSCPPGYILLDDNRSCQDINECEHRNHTCNLQQTTCYNLQGGFKCIDPIRCEEPYL	300
Db	266	PGTYFCSCPPGYILLDDNRSCQDINECEHRNHTCNLQQTTCYNLQGGFKCIDPIRCEEPYL	325
Qy	301	RISDNRCMCPAENPGCRDQPFTILYRDMDVVSGRSVPADIFQMQATTRYPGAYYIFQIKS	360
Db	326	RISDNRCMCPAENPGCRDQPFTILYRDMDVVSGRSVPADIFQMQATTRYPGAYYIFQIKS	385
Qy	361	GNEGREFYMRQTGPISATLVMTRPIKGPRIQLDLEMITVNTVINFRGSSVIRLRIYVSQ	420
Db	386	GNEGREFYMRQTGPISATLVMTRPIKGPRIQLDLEMITVNTVINFRGSSVIRLRIYVSQ	445
Qy	421	YPF	423
Db	446	YPF	448

RESULT 3

AAW94281

ID AAW94281 standard; Protein; 448 AA.

XX

AC AAW94281;

XX

DT 07-MAY-1999 (first entry)

XX

DE Human extracellular matrix protein (ECMP)-1.

XX

KW Extracellular matrix protein; ECMP-1; diagnosis; treatment; cancer;
 KW immune disorder; human.

XX

OS Homo sapiens.

XX

PN WO9900410-A2.

XX

PD 07-JAN-1999.

XX

PF 23-JUN-1998; 98WO-US13012.

XX
 PR 27-JUN-1997; 97US-0884072.
 XX
 PA (INCY-) INCYTE PHARM INC.
 XX
 PI Bandman O, Corley NC, Guegler KJ;
 XX
 DR WPI; 1999-095674/08.
 DR N-PSDB; AAX05359.
 XX
 PT New polynucleotide encoding extracellular matrix protein, ECMP-1 -
 PT useful in the diagnosis, prevention and treatment of immune
 PT disorders and cancer
 XX
 PS Claim 1; Fig 1A-G; 79pp; English.
 XX
 CC This represents a human extracellular matrix protein (ECMP)-1. Host
 CC cells containing a vector comprising the ECMP-1 nucleic acid are used
 CC for the recombinant production of the protein. ECMP-1 and its
 CC (ant)agonists, are useful in the diagnosis, prevention, and treatment
 CC of cancer and immune disorders.
 XX
 SQ Sequence 448 AA;

Query Match 100.0%; Score 2407; DB 20; Length 448;
 Best Local Similarity 100.0%; Pred. No. 1.2e-159;
 Matches 423; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	QCTNGFDLDRQSGQCLDIDECRTIPEACRGDMMCVNQNGGYLCIPRTNPVYRGPYSNPYS	60
Db	26	QCTNGFDLDRQSGQCLDIDECRTIPEACRGDMMCVNQNGGYLCIPRTNPVYRGPYSNPYS	85
Qy	61	TPYSGPYPAAAPPLSAPNYPTISRPLICRFGYQMDASNQCVDVDECATDSHQCNPQTQICI	120
Db	86	TPYSGPYPAAAPPLSAPNYPTISRPLICRFGYQMDASNQCVDVDECATDSHQCNPQTQICI	145
Qy	121	NTEGGYTCSCTDGYWLLEGQCLDIDECRYGYCQQLCANVPGSYSCTCNPGFTLNEDGRSC	180
Db	146	NTEGGYTCSCTDGYWLLEGQCLDIDECRYGYCQQLCANVPGSYSCTCNPGFTLNEDGRSC	205
Qy	181	QDVNECATENPCVQTCVNTYGSFICRCDPGYELEEDGVHCSDMDECSFSEFLCQHECVNQ	240
Db	206	QDVNECATENPCVQTCVNTYGSFICRCDPGYELEEDGVHCSDMDECSFSEFLCQHECVNQ	265
Qy	241	PGTYFCSCPPGYILLDDNRSCQDINECEHRNHTCNLQQTCYNLQGGFKCIDPIRCEEPYL	300
Db	266	PGTYFCSCPPGYILLDDNRSCQDINECEHRNHTCNLQQTCYNLQGGFKCIDPIRCEEPYL	325
Qy	301	RISDNRCMCPAENPGCRDQPFITILYRDMDVVSGRSVPADIFQMQATTRYPGAYYIFQIKS	360
Db	326	RISDNRCMCPAENPGCRDQPFITILYRDMDVVSGRSVPADIFQMQATTRYPGAYYIFQIKS	385
Qy	361	GNEGREFYMRQTGPISATLVMTRPIKGPREIQLDLEMITVNTVINFRGSSVIRLRIYVSQ	420
Db	386	GNEGREFYMRQTGPISATLVMTRPIKGPREIQLDLEMITVNTVINFRGSSVIRLRIYVSQ	445
Qy	421	YPF	423

Db

446 YPF 448

RESULT 4

AAY57058

ID AAY57058 standard; Protein; 448 AA.

XX

AC AAY57058;

XX

DT 21-FEB-2000 (first entry)

XX

DE Amino acid sequence of the human secreted protein AK647.

XX

KW AK647; aortic tissue development; smooth muscle cell modulator; SCID;
KW nutritional supplement; vasculogenesis; embryonic development; infection;
KW cytokine activity; cell proliferation; cell differentiation; detect; HIV;
KW immune deficiency; haematopoiesis regulation; tissue regrowth; diagnose;
KW wound healing; restenosis; atherosclerosis; drug screen.

XX

OS Homo sapiens.

XX

PN WO9960125-A2.

XX

PD 25-NOV-1999.

XX

PF 18-MAY-1999; 99WO-US10931.

XX

PR 19-MAY-1998; 98US-0081002.

PR 21-MAY-1998; 98US-0083002.

XX

PA (GEMY) GENETICS INST INC.

XX

PI Jacobs K, McCoy JM, Racie L, LaVallie E, Treacy M, Evans C;
PI Agostino M, Lu Z, Merberg D;

XX

DR WPI; 2000-053298/04.

DR N-PSDB; AAZ39892.

XX

PT Proteins, and their encoding polynucleotides, used for treating e.g.
PT smooth muscle cell growth, vasculogenesis, restenosis or
PT atherosclerosis -

XX

PS Claim 4; Page 46-47; 49pp; English.

XX

CC This is the amino acid sequence of the human secreted protein AK647. The
CC polynucleotide sequence was obtained from a human foetal kidney cDNA
CC library. AK647 homologues in chicks and rodents are involved in aortic
CC tissue development. The spatial and temporal distribution of AK647
CC indicated that it acts as an a modulator of smooth muscle cells in
CC vasculogenesis during embryonic development. The primary structure of
CC AK647 consists of multiple EGF domains. The AK647 protein can be used as
CC a nutritional source or supplement. The protein shows both inhibitory and
CC inducing, cytokine, cell proliferation and cell differentiation activity.
CC The protein may also be used in the treatment of immune deficiencies and
CC disorders, including severe combined immunodeficiency (SCID), HIV and
CC other viral, bacterial and fungal infections. Regulation of immune

XX
 AC AAY54989;
 XX
 DT 15-FEB-2000 (first entry)
 XX
 DE Full length human A55 protein sequence.
 XX
 KW A55 protein; human; smooth muscle proliferation; tissue generation;
 KW vascular smooth muscle cell; arteriosclerosis; tissue reparation; myoma;
 KW vascular endothelial thickening; haematopoietic cell-regulator; cytokine;
 KW percutaneous transluminal coronary angioplasty; blood coagulation; PTCA;
 KW actin; inhibin; chemotaxis; thrombosis; cadherin; therapy;
 KW tumour metastasis inhibitor.
 XX
 OS Homo sapiens.
 XX
 PN WO9955864-A1.
 XX
 PD 04-NOV-1999.
 XX
 PF 28-APR-1999; 99WO-JP02284.
 XX
 PR 28-APR-1998; 98JP-0119731.
 XX
 PA (ONOEY) ONO PHARM CO LTD.
 XX
 PI Honjo T, Tashiro K, Nakamura T;
 XX
 DR WPI; 2000-038647/03.
 DR N-PSDB; AAZ40027.
 XX
 PT Novel human polypeptides for treatment of, e.g. arteriosclerosis and
 PT myoma -
 XX
 PS Claim 1; Page 76-80; 87pp; Japanese.
 XX
 CC This sequence is the human A55 protein of the invention. The protein
 CC can be used for the treatment of diseases due to abnormal proliferation
 CC of smooth muscle. The polypeptides can be used according their inhibition
 CC of the proliferation of vascular smooth muscle cells, particularly in
 CC treating arteriosclerosis or re-narrowing by vascular endothelial
 CC thickening after percutaneous transluminal coronary angioplasty (PTCA),
 CC or myoma, haematopoietic cell-regulatory activity, cytokine activity,
 CC tissue generation/reparation activity, actin/inhibin activity, taxis
 CC and chemotaxis activity, blood coagulation/thrombotic activity,
 CC receptor/ligand activity, cadherin/tumour metastasis inhibiting activity;
 CC tumour inhibition, and as a nutrient.
 XX
 SQ Sequence 448 AA;

Query Match 100.0%; Score 2407; DB 21; Length 448;
 Best Local Similarity 100.0%; Pred. No. 1.2e-159;
 Matches 423; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QCTNGFDLDRQSGQCLDIDECRTIPEACRGDMMCVNQGGYLCIPRTNPVYRGPYSNPYS 60
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 26 QCTNGFDLDRQSGQCLDIDECRTIPEACRGDMMCVNQGGYLCIPRTNPVYRGPYSNPYS 85

Qy	61	TPYSGPYPAAPPLSAPNYPTISRPLICRFGYQMDESNCVDVDECATDSHQCNPQTQICI	120
Db	86	TPYSGPYPAAPPLSAPNYPTISRPLICRFGYQMDESNCVDVDECATDSHQCNPQTQICI	145
Qy	121	NTEGGYTCSCTDGYWLLEGQCLDIDECRYGYCQQLCANVPGSYSCTCNPGFTLNEDGRSC	180
Db	146	NTEGGYTCSCTDGYWLLEGQCLDIDECRYGYCQQLCANVPGSYSCTCNPGFTLNEDGRSC	205
Qy	181	QDVNECATENPCVQTCVNTYGSFICRCDPGYELEEDGVHCSDMDECSFSEFLCQHECVNQ	240
Db	206	QDVNECATENPCVQTCVNTYGSFICRCDPGYELEEDGVHCSDMDECSFSEFLCQHECVNQ	265
Qy	241	PGTYFCSCPPGYILLDDNRSCQDINECEHRNHTCNLQQTTCYNLQGGFKCIDPIRCEEPYL	300
Db	266	PGTYFCSCPPGYILLDDNRSCQDINECEHRNHTCNLQQTTCYNLQGGFKCIDPIRCEEPYL	325
Qy	301	RISDNRCMCPAENPGCRDQPFTILYRDMDVVSGRSVPADIFQMQATTRYPGAYYIFQIKS	360
Db	326	RISDNRCMCPAENPGCRDQPFTILYRDMDVVSGRSVPADIFQMQATTRYPGAYYIFQIKS	385
Qy	361	GNEGREFYMRQTGPISATLVMTRPIKGPRIQLDLEMITVNTVINFRGSSVIRLRIYVSQ	420
Db	386	GNEGREFYMRQTGPISATLVMTRPIKGPRIQLDLEMITVNTVINFRGSSVIRLRIYVSQ	445
Qy	421	YPF	423
Db	446	YPF	448

RESULT 6

AAM93573

ID AAM93573 standard; Protein; 448 AA.

XX

AC AAM93573;

XX

DT 06-NOV-2001 (first entry)

XX

DE Human polypeptide, SEQ ID NO: 3357.

XX

KW Human; full length cDNA; cDNA synthesis; oligo-capping.

XX

OS Homo sapiens.

XX

PN EP1130094-A2.

XX

PD 05-SEP-2001.

XX

PF 07-JUL-2000; 2000EP-0114089.

XX

PR 08-JUL-1999; 99JP-0194486.

PR 11-JAN-2000; 2000JP-0118774.

PR 02-MAY-2000; 2000JP-0183765.

XX

PA (HELI-) HELIX RES INST.

XX

PI Ota T, Nishikawa T, Isogai T, Hayashi K, Ishii S, Kawai Y;

PI Wakamatsu A, Sugiyama T, Nagai K, Kojima S, Otsuki T, Koga H;
 XX
 DR WPI; 2001-524255/58.
 DR N-PSDB; AAK94505.
 XX
 PT 830 Primers useful for synthesizing full length cDNA clones and their
 PT use in genetic manipulation -
 XX
 PS Claim 8; SEQ ID NO 3357; 1380pp + sequence listing; English.
 XX
 CC The invention relates to primers for synthesising full length cDNA
 CC clones. 830 cDNA molecules encoding a human protein have been
 CC isolated and nucleotide sequences of 5'- and 3'-ends of the cDNA
 CC molecules have been determined. Primers for synthesising the full length
 CC cDNA are useful for clarifying the function of the protein encoded by
 CC the cDNA. The full length clones were obtained by construction of full
 CC length enriched cDNA libraries that were synthesised by the oligo-capping
 CC method. The primers enable the production of the full length cDNA easily
 CC without any special methods. The present sequence is a polypeptide
 CC encoded by a full length human cDNA of the invention.
 CC Note: The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in CD-ROM format directly from EPO.
 XX
 SQ Sequence 448 AA;

Query Match 100.0%; Score 2407; DB 22; Length 448;
 Best Local Similarity 100.0%; Pred. No. 1.2e-159;
 Matches 423; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	QCTNGFDLDRQSGQCLDIDECRTIPEACRGDMMCVNQNGGYLCIPRTNPVYRGYPYNSNPYS	60
Db	26	QCTNGFDLDRQSGQCLDIDECRTIPEACRGDMMCVNQNGGYLCIPRTNPVYRGYPYNSNPYS	85
Qy	61	TPYSGPYPAAAPPLSAPNYPTISRPLICRFGYQMDASNQCVDVDECATDSHQCNPTQICICI	120
Db	86	TPYSGPYPAAAPPLSAPNYPTISRPLICRFGYQMDASNQCVDVDECATDSHQCNPTQICICI	145
Qy	121	NTEGGYTCSCCTDGYWLLEGQCLDIDECRYGYCQQLCANVPGSYSCTCNPGFTLNEDGRSC	180
Db	146	NTEGGYTCSCCTDGYWLLEGQCLDIDECRYGYCQQLCANVPGSYSCTCNPGFTLNEDGRSC	205
Qy	181	QDVNECATENPCVQTCVNTYGSFICRCDPGYELEEDGVHCSDMDECSFSEFLCQHECVNQ	240
Db	206	QDVNECATENPCVQTCVNTYGSFICRCDPGYELEEDGVHCSDMDECSFSEFLCQHECVNQ	265
Qy	241	PGTYFCSCPPGYILLDDNRSCQDINECEHRNHTCNLQQTCYNLQGGFKCIDPIRCEEPYL	300
Db	266	PGTYFCSCPPGYILLDDNRSCQDINECEHRNHTCNLQQTCYNLQGGFKCIDPIRCEEPYL	325
Qy	301	RISDNRCMCPAENPGCRDQPFITILYRDMDVVSGRSVPADIFQMQATTRYPGAYYIFQIKS	360
Db	326	RISDNRCMCPAENPGCRDQPFITILYRDMDVVSGRSVPADIFQMQATTRYPGAYYIFQIKS	385
Qy	361	GNEGREFYMRQTGPISATLVMTRPIKGPRIQLDLEMITVNTVINFRGSSVIRLRIYVSQ	420
Db	386	GNEGREFYMRQTGPISATLVMTRPIKGPRIQLDLEMITVNTVINFRGSSVIRLRIYVSQ	445

Qy 421 YPF 423
|||
Db 446 YPF 448

RESULT 7

AAU75494

ID AAU75494 standard; Protein; 448 AA.

XX

AC AAU75494;

XX

DT 23-APR-2002 (first entry)

XX

DE Human extracellular protein-like/EGF-like protein, EEGF.

XX

KW Human; extracellular protein-like protein; EGF-like;
KW protein; epidermal growth factor; EEGF; ATCC 97285; gene therapy;
KW vascular smooth muscle cell proliferation; Marfan syndrome;
KW wound healing; neurological trauma; acquired immunodeficiency syndrome;
KW AIDS-related dementia; ocular disorder; kidney disorder; liver disorder;
KW hair follicle growth promotion; burn; ulcer; corneal incision;
KW corneal inflammation; neoplasm; psoriasis.

XX

OS Homo sapiens.

XX

FH Key Location/Qualifiers

FT Peptide 1..25

FT /label= Signal_peptide

FT Protein 26..448

FT /label= Mature_EEGF

FT /note= "This region is specifically claimed in claim 10"

FT Domain 112..153

FT /label= EGF_1_domain

FT /note= "This domain is specifically claimed in claim 10"

FT Domain 154..190

FT /label= EGF_2_domain

FT /note= "This domain is specifically claimed in claim 10"

FT Domain 191..230

FT /label= EGF_3_domain

FT /note= "This domain is specifically claimed in claim 10"

FT Domain 231..271

FT /label= EGF_4_domain

FT /note= "This domain is specifically claimed in claim 10"

FT Domain 272..314

FT /label= EGF_5_domain

FT /note= "This domain is specifically claimed in claim 10"

XX

PN US2001051358-A1.

XX

PD 13-DEC-2001.

XX

PF 25-MAR-1999; 99US-0275805.

XX

PR 11-APR-1997; 97US-0839525.

PR 10-APR-1996; 96WO-US05247.

XX

PA (OLSE/) OLSEN H S.

Qy	301	RISDNRCMCPAENPGCRDQPF	TILYRDMDVVSGRSVPADIFQM	QATTRYPGAYYIFQIKS	360
Db	326	RISDNRCMCPAENPGCRDQPF	TILYRDMDVVSGRSVPADIFQM	QATTRYPGAYYIFQIKS	385
Qy	361	GNEGREFYMRQTGPISATLVM	TRPIKGP	PREIQLDLEM	ITVNTVINFRGSSVIRLRIYVSQ
Db	386	GNEGREFYMRQTGPISATLVM	TRPIKGP	PREIQLDLEM	ITVNTVINFRGSSVIRLRIYVSQ
Qy	421	YPF	423		
Db	446	YPF	448		

RESULT 8

AAAY08063

ID AAY08063 standard; Protein; 448 AA.

XX

AC AAY08063;

XX

DT 11-SEP-2000 (first entry)

XX

DE Human EGF-like homologue protein (PRO217) encoded by DNA32279 cDNA.

XX

KW Inflammatory cell infiltration; immune response; T cell proliferation;
 KW anti-inflammatory; anti-autoimmune; anti-diabetic; spondyloarthropathy;
 KW T cell-mediated disease; spondyloarthropathy; sclerosis; renal disease;
 KW inflammatory myopathy; hemolytic anemia; thrombocytopenia; thyroiditis;
 KW diabetes mellitus; demyelinating polyneuropathy; Guillain-Barre syndrome;
 KW multiple sclerosis; polyneuropathy; hepatitis; cirrhosis; enteropathy;
 KW sclerosing cholangitis; inflammatory bowel disease; Whipple's disease;
 KW skin disease; dermatitis; psoriasis; asthma; allergic rhinitis; tumor;
 KW food hypersensitivity; urticaria; eosinophilic pneumonia; transplant;
 KW idiopathic pulmonary fibrosis; graft rejection; PRO245; human; PRO217;
 KW EGF-like.

XX

OS Homo sapiens.

XX

PN WO9914241-A2.

XX

PD 25-MAR-1999.

XX

PF 17-SEP-1998; 98WO-US19437.

XX

PR 17-SEP-1997; 97US-0059119.

PR 18-SEP-1997; 97US-0059263.

PR 28-OCT-1997; 97US-0063550.

PR 12-NOV-1997; 97US-0065186.

PR 21-NOV-1997; 97US-0066364.

PR 24-NOV-1997; 97US-0066770.

PR 04-JUN-1998; 98US-0088026.

XX

PA (GETH) GENENTECH INC.

XX

PI Fong S, Goddard A, Gurney AL, Tumas D, Wood WI;

XX

DR WPI; 1999-229499/19.

DR N-PSDB; AAX37670.

XX

PT Composition containing novel polypeptide PRO245, its agonist or
PT antagonist -

XX

PS Example 1; Fig 6A; 177pp; English.

XX

CC This invention describes a novel composition containing (apart from a
CC carrier or excipient), a novel PRO245 polypeptide (I), its agonist or
CC antagonist, or their fragments, for modulating: (i) infiltration of
CC inflammatory cells into tissue; (ii) an immune response; or (iii) T cell
CC proliferation. The composition increases or decreases any of the effects
CC (i)-(iii). The products of the invention have anti-inflammatory,
CC anti-autoimmune and anti-diabetic activity. (I), and its (ant)agonists
CC and their fragments, are used to treat immune-related diseases,
CC particularly T cell-mediated diseases. The diseases treated include
CC systemic lupus erythematosus, rheumatoid arthritis, juvenile chronic
CC arthritis, spondyloarthropathies, systemic sclerosis (scleroderma),
CC idiopathic inflammatory myopathies (dermatomyositis, polymyositis),
CC Sjogren's syndrome, systemic vasculitis, sarcoidosis, autoimmune
CC hemolytic anemia (immune pancytopenia, paroxysmal nocturnal
CC hemoglobinuria), autoimmune thrombocytopenia (idiopathic thrombocytopenic
CC purpura immune-mediated thrombocytopenia), thyroiditis (Grave's disease,
CC Hashimoto's thyroiditis, juvenile lymphocytic thyroiditis, atrophic
CC thyroiditis), diabetes mellitus, immune-mediated renal disease
CC (glomerulonephritis, tubulointerstitial nephritis), multiple sclerosis,
CC idiopathic demyelinating polyneuropathy, Guillain-Barre syndrome, chronic
CC inflammatory demyelinating polyneuropathy, infectious hepatitis
CC (hepatitis A, B, C, D, E and other non-hepatotropic viruses), autoimmune
CC chronic active hepatitis, primary biliary cirrhosis, granulomatous
CC hepatitis, and sclerosing cholangitis, inflammatory bowel disease
CC (ulcerative colitis: Crohn's disease), gluten-sensitive enteropathy, and
CC Whipple's disease. Autoimmune or immune-mediated skin diseases including
CC bullous skin diseases, erythema multiforme, contact dermatitis, psoriasis,
CC asthma, allergic rhinitis, atopic dermatitis, food hypersensitivity,
CC urticaria, eosinophilic pneumonia, idiopathic pulmonary fibrosis,
CC hypersensitivity pneumonitis, and transplantation associated diseases
CC (graft rejection, and graft-versus-host-disease). (I), its (ant)agonists
CC or fragment can also be used as an adjuvant in treatment of tumors.
CC Antibodies against (I) can also be used for diagnosing such diseases.
CC This sequence represents a human EGF-like homologue encoded by cDNA clone
CC DNA32279 which is described in the invention.

XX

SQ Sequence 448 AA;

Query Match 99.8%; Score 2401; DB 20; Length 448;
Best Local Similarity 99.8%; Pred. No. 3.2e-159;
Matches 422; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QCTNGFDLDRQSGQCLDIDECRTIPEACRGDMMCVNQNGGYLCIPRTNPVYRGYPYNSPYS 60
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 26 QCTNGFDLDRQSGQCLDIDECRTIPEACRGDMMCVNQNGGYLCIPRTNPVYRGYPYNSPYS 85
Qy 61 TPYSGPYPAAPPLSAPNYPTISRPLICRFGYQMDASNQCVDVDECATDSHCNPTQICICI 120
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 86 TPYSGPYPAAPPLSAPNYPTISRPLICRFGYQMDASNQCVDVDECATDSHCNPTQICICI 145
Qy 121 NTEGGYTCSCTDGYWLLEGQCLDIDECRYGYCQQLCANVPGSYSCTCNPGFTLNEDGRSC 180

Db	146		NTGGYTCSC	TDGYW	LEGQCLDI	DECRYGYCQQLCANVPGSYSCTCNPGFTLNEDGRSC	205
Qy	181		QDVNECATENPCVQTCVNTYGSFICRCDPGYELEEDGVHCSDMDECSFSEFLCQHECVNQ	240			
Db	206		QDVNECATENPCVQTCVNTYGSFICRCDPGYELEEDGVHCSDMDECSFSEFLCQHECVNQ	265			
Qy	241		PGTYFCSCPPGYILLDDNRSCQDINECEHRNHTCNLQQTTCYNLQGGFKCIDPIRCEEPYL	300			
Db	266		PGTYFCSCPPGYILLDDNRSCQDINECEHRNHTCNLQQTTCYNLQGGFKCIDPIRCEEPYL	325			
Qy	301		RISDNRCMCPAENPGCRDQPFTILYRDMDVVSGRSVPADIFQMQATTRYPGAYYIFQIKS	360			
Db	326		RISDNRCMCPAENPGCRDQPFTILYRDMDVVSGRSVPADIFQMQATTRYPGAYYIFQIKS	385			
Qy	361		GNEGREFYMRQTGPISATLVMTRPIKGPRIQLDLEMITVNTVINFRGSSVIRLRIYVSQ	420			
Db	386		GNEGREFYMRQTGPISATLVMTRPIKGPRIQLDLEMITVNTVINFRGSSVIRLRIYVSQ	445			
Qy	421		YPF	423			
Db	446		YPF	448			

RESULT 9

AAU29227

ID AAU29227 standard; Protein; 448 AA.

XX

AC AAU29227;

XX

DT 18-DEC-2001 (first entry)

XX

DE Human PRO polypeptide sequence #204.

XX

KW PRO polypeptide; mammal; tumour; cancer; human; cattle; horse; sheep;
 KW dog; cat; pig; goat; rabbit; tumour necrosis factor alpha; TNF-alpha;
 KW blood; chondrocyte cell; cell proliferation; cell differentiation; colon;
 KW adrenal; lung; breast; prostate; rectum; cervix; liver; genetic disorder.

XX

OS Homo sapiens.

XX

PN WO200168848-A2.

XX

PD 20-SEP-2001.

XX

PF 28-FEB-2001; 2001WO-US06520.

XX

PR 01-MAR-2000; 2000WO-US05601.

PR 02-MAR-2000; 2000WO-US05841.

PR 03-MAR-2000; 2000US-187202P.

PR 06-MAR-2000; 2000US-186968P.

PR 14-MAR-2000; 2000US-189320P.

PR 14-MAR-2000; 2000US-189328P.

PR 15-MAR-2000; 2000WO-US06884.

PR 21-MAR-2000; 2000US-190828P.

PR 21-MAR-2000; 2000US-191007P.

PR 21-MAR-2000; 2000US-191048P.

PR 21-MAR-2000; 2000US-191314P.
PR 28-MAR-2000; 2000US-192655P.
PR 29-MAR-2000; 2000US-193032P.
PR 29-MAR-2000; 2000US-193053P.
PR 30-MAR-2000; 2000WO-US08439.
PR 04-APR-2000; 2000US-194449P.
PR 04-APR-2000; 2000US-194647P.
PR 11-APR-2000; 2000US-195975P.
PR 11-APR-2000; 2000US-196000P.
PR 11-APR-2000; 2000US-196187P.
PR 11-APR-2000; 2000US-196690P.
PR 11-APR-2000; 2000US-196820P.
PR 18-APR-2000; 2000US-198121P.
PR 18-APR-2000; 2000US-198585P.
PR 25-APR-2000; 2000US-199397P.
PR 25-APR-2000; 2000US-199550P.
PR 25-APR-2000; 2000US-199654P.
PR 03-MAY-2000; 2000US-201516P.
PR 17-MAY-2000; 2000WO-US13705.
PR 22-MAY-2000; 2000WO-US14042.
PR 30-MAY-2000; 2000WO-US14941.
PR 02-JUN-2000; 2000WO-US15264.
PR 05-JUN-2000; 2000US-209832P.
PR 28-JUL-2000; 2000WO-US20710.
PR 22-AUG-2000; 2000US-0644848.
PR 24-AUG-2000; 2000WO-US23328.
PR 08-NOV-2000; 2000WO-US30952.
PR 01-DEC-2000; 2000WO-US32678.
PR 20-DEC-2000; 2000WO-US34956.

XX

PA (GETH) GENENTECH INC.

XX

PI Baker KP, Chen J, Desnoyers L, Goddard A, Godowski PJ, Gurney AL;
PI Pan J, Smith V, Watanabe CK, Wood WI, Zhang Z;

XX

DR WPI; 2001-602746/68.

DR N-PSDB; AAS46128.

XX

PT Novel nucleic acids encoding PRO polypeptides, used to diagnose the
PT presence of tumours, such as prostate and breast tumours, in mammals and
PT to screen for modulators of the compounds -

XX

PS Claim 11; Fig 408; 774pp; English.

XX

CC Sequences AAU29024-AAU29328 represent PRO polypeptides of the invention.
CC The PRO polypeptides and their associated nucleic acids can be used to
CC detect the presence of a tumour in a mammal by comparing the level of
CC expression of a PRO polypeptide in a test sample of cells from the animal
CC and a control sample of normal cells, whereby a higher level of
CC expression in the test sample indicates the presence of a tumour in the
CC mammal. Mammals include dogs, cats, cattle, horses, sheep, pigs, goats
CC and rabbits but are preferably human. The polypeptides can be used to
CC stimulate tumour necrosis factor (TNF) alpha release from human blood,
CC when contacted with it. A specific polypeptide can be used to stimulate
CC the proliferation or differentiation of chondrocyte cells. The PRO
CC proteins can be used to determine the presence of tumours and also
CC susceptibility to tumour development, particularly adrenal, lung, colon,

CC breast, prostate, rectal, cervical, or liver tumours, in mammalian
CC subjects. The oligonucleotide probes specific for the PRO nucleic acids
CC can be used for genetic analysis of individuals with genetic disorders.

XX

SQ Sequence 448 AA;

Query Match 99.8%; Score 2401; DB 22; Length 448;
Best Local Similarity 99.8%; Pred. No. 3.2e-159;
Matches 422; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```
Qy      1 QCTNGFDLDRQSGQCLDIDECRTIPEACRGDMMCVNQNGGYLCIPRTNPVYRGPYSNPYS 60
      |||
Db      26 QCTNGFDLDRQSGQCLDIDECRTIPEACRGDMMCVNQNGGYLCIPRTNPVYRGPYSNPYS 85

Qy     61 TPYSGPYPAAPPLSAPNYPTISRPLICRFGYQMDESNQCVDVDECATDSHCNPTQICI 120
      |||
Db     86 TPYSGPYPAAPPLSAPNYPTISRPLICRFGYQMDESNQCVDVDECATDSHCNPTQICI 145

Qy    121 NTEGGYTCSCTDGYWLLEGQCLDIDECRYGYCQQLCANVPGSYSCTCNPGFTLNEDGRSC 180
      |||
Db    146 NTEGGYTCSCTDGYWLLEGQCLDIDECRYGYCQQLCANVPGSYSCTCNPGFTLNEDGRSC 205

Qy    181 QDVNECATENPCVQTCVNTYGSFICRCDPGYELEEDGVHCSDMDECSFSEFLCQHECVNQ 240
      |||
Db    206 QDVNECATENPCVQTCVNTYGSFICRCDPGYELEEDGVHCSDMDECSFSEFLCQHECVNQ 265

Qy    241 PGTYFCSCPPGYILLDDNRSCQDINECEHRNHTCNLQQTTCYNLQGGFKCIDPIRCEEPYL 300
      |||
Db    266 PGTYFCSCPPGYILLDDNRSCQDINECEHRNHTCNLQQTTCYNLQGGFKCIDPIRCEEPYL 325

Qy    301 RISDNRCMCPAENPGCRDQPFTILYRDMDVVSGRSVPADIFQMQATTRYPGAYYIFQIKS 360
      |||
Db    326 RISDNRCMCPAENPGCRDQPFTILYRDMDVVSGRSVPADIFQMQATTRYPGAYYIFQIKS 385

Qy    361 GNEGREFYMRQTGPISATLVMTRPIKGPREIQLDLEMITVNTVINFRGSSVIRLRIYVSQ 420
      |||
Db    386 GNEGREFYMRQTGPISATLVMTRPIKGPREIQLDLEMITVNTVINFRGSSVIRLRIYVSQ 445

Qy    421 YPF 423
      |||
Db    446 YPF 448
```

RESULT 10

AAB31183

ID AAB31183 standard; Protein; 448 AA.

XX

AC AAB31183;

XX

DT 20-APR-2001 (first entry)

XX

DE Amino acid sequence of human polypeptide PRO210.

XX

KW Human; secreted protein; transmembrane protein; PRO196; PRO444; PRO183;

KW PRO185; PRO210; PRO215; PRO217; PRO242; PRO288; PRO365; PRO1361; PRO1308;

KW PRO1183; PRO1272; PRO1419; PRO4999; PRO7170; PRO248; PRO353; PRO1318;

KW PRO1600; PRO9940; PRO533; PRO301; PRO187; PRO337; PRO1411; PRO4356;

KW PRO246; PRO265; PRO941; PRO10096; PRO6003; PRO6004; PRO350; PRO2630;
 KW PRO6309; cell death; genetic disorder; transgenic animal; gene therapy.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Peptide 1..25
 FT /note= "signal peptide"
 FT Modified-site 21..27
 FT /note= "N-myristoylation site"
 FT Binding-site 54..57
 FT /note= "cell attachment site"
 FT Modified-site 64..70
 FT /note= "N-myristoylation site"
 FT Modified-site 144..156
 FT /note= "aspartic acid and asparagine hydroxylation site"
 FT Modified-site 149..155
 FT /note= "N-myristoylation site"
 FT Modified-site 186..192
 FT /note= "N-myristoylation site"
 FT Modified-site 226..232
 FT /note= "N-myristoylation site"
 FT Modified-site 242..248
 FT /note= "N-myristoylation site"
 FT Modified-site 267..273
 FT /note= "N-myristoylation site"
 FT Modified-site 283..287
 FT /note= "N-glycosylation site"
 FT Modified-site 296..300
 FT /note= "N-glycosylation site"
 FT Modified-site 310..316
 FT /note= "N-myristoylation site"
 XX
 PN WO200077037-A2.
 XX
 PD 21-DEC-2000.
 XX
 PF 22-MAY-2000; 2000WO-US14042.
 XX
 PR 15-JUN-1999; 99US-0139695.
 PR 20-JUL-1999; 99US-0145070.
 PR 26-JUL-1999; 99US-0145698.
 PR 17-AUG-1999; 99US-0149396.
 PR 01-SEP-1999; 99WO-US20111.
 PR 08-SEP-1999; 99WO-US20594.
 PR 15-SEP-1999; 99WO-US21090.
 PR 15-SEP-1999; 99WO-US21547.
 PR 30-NOV-1999; 99WO-US28313.
 PR 01-DEC-1999; 99WO-US28301.
 PR 02-DEC-1999; 99WO-US28565.
 PR 07-DEC-1999; 99US-0169495.
 PR 05-JAN-2000; 2000WO-US00219.
 PR 18-FEB-2000; 2000WO-US04341.
 PR 18-FEB-2000; 2000WO-US04342.
 PR 22-FEB-2000; 2000WO-US04414.
 PR 01-MAR-2000; 2000WO-US05601.
 PR 02-MAR-2000; 2000WO-US05841.

PR 20-MAR-2000; 2000WO-US07377.
PR 30-MAR-2000; 2000WO-US08439.
PR 15-MAY-2000; 2000WO-US13358.
PR 17-MAY-2000; 2000WO-US13705.

XX

PA (GETH) GENENTECH INC.

XX

PI Ashkenazi AJ, Baker KP, Botstein DA, Desnoyers L, Eaton DL;
PI Ferrara N, Fong S, Gao W, Gerber H, Gerritsen ME, Goddard A;
PI Godowski PJ, Gurney AL, Kljavin IJ, Mather JP, Napier MA, Pan J;
PI Paoni NF, Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PM;
PI Wood WI, Zhang Z;

XX

DR WPI; 2001-050091/06.

DR N-PSDB; AAC86968.

XX

PT Isolated nucleic acid molecule encoding a PRO polypeptide which is a
PT transmembrane polypeptide is useful for gene therapy and identification
PT of related polypeptides -

XX

PS Claim 12; Fig 10; 244pp; English.

XX

CC The present sequence represents a human secreted and transmembrane
CC polypeptide. The specification describes human polypeptides, designated
CC PRO196, PRO444, PRO183, PRO185, PRO210, PRO215, PRO217, PRO242, PRO288,
CC PRO365, PRO1361, PRO1308, PRO1183, PRO1272, PRO1419, PRO4999, PRO7170,
CC PRO248, PRO353, PRO1318, PRO1600, PRO9940, PRO533, PRO301, PRO187,
CC PRO337, PRO1411, PRO4356, PRO246, PRO265, PRO941, PRO10096, PRO6003,
CC PRO6004, PRO350, PRO2630 and PRO6309. The biological activity of cells
CC can be modulated with agents that bind to these polypeptides, resulting
CC in the death of the cells. The polynucleotides encoding these
CC polypeptides are useful in the recombinant production of the
CC polypeptides, as a hybridisation probe to screen libraries to isolate
CC homologous sequences, or to map the gene. They may also be used for
CC analysing genetic disorders, and to produce transgenic animals which are
CC useful for the development and screening of therapeutically useful
CC reagents. The polynucleotides can also be used in gene therapy e.g. to
CC replace a defective gene.

XX

SQ Sequence 448 AA;

Query Match 99.8%; Score 2401; DB 22; Length 448;
Best Local Similarity 99.8%; Pred. No. 3.2e-159;
Matches 422; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy	1	QCTNGFDLDRQSGQCLDIDECRTIPEACRGDMMCVNQNGGYLCIPRTNPVYRGPYSNPYS	60
Db	26	QCTNGFDLDRQSGQCLDIDECRTIPEACRGDMMCVNQNGGYLCIPRTNPVYRGPYSNPYS	85
Qy	61	TPYSGPYPAAPPLSAPNYPTISRPLICRFGYQMDESNQCVDVDECATDSHQCNPTQICI	120
Db	86	TPYSGPYPAAPPLSAPNYPTISRPLICRFGYQMDESNQCVDVDECATDSHQCNPTQICI	145
Qy	121	NTEGGYTCSCTDGYWLLEGQCLDIDECRYGYCQQLCANVPGSYSCTCNPGF TLNEDGRSC	180
Db	146	NTEGGYTCSCTDGYWLLEGQCLDIDECRYGYCQQLCANVPGSYSCTCNPGF TLNEDGRSC	205

Qy	181	QDVNECATENPCVQTCVNTYGSFICRCDPGYELEEDGVHCSDMDECSFSEFLCQHECVNQ	240
Db	206	QDVNECATENPCVQTCVNTYGLICRCDPGYELEEDGVHCSDMDECSFSEFLCQHECVNQ	265
Qy	241	PGTYFCSCPPGYILLDDNRSCQDINECEHRNHTCNLQQTCYNLQGGFKCIDPIRCEEPYL	300
Db	266	PGTYFCSCPPGYILLDDNRSCQDINECEHRNHTCNLQQTCYNLQGGFKCIDPIRCEEPYL	325
Qy	301	RISDNRCMCPAENPGCRDQPFTILYRDMDVVSGRSVPADIFQMQATTRYPGAYYIFQIKS	360
Db	326	RISDNRCMCPAENPGCRDQPFTILYRDMDVVSGRSVPADIFQMQATTRYPGAYYIFQIKS	385
Qy	361	GNEGREFYMRQTGPISATLMTRPIKGPREIQLDLEMITVNTVINFRGSSVIRLRIYVSQ	420
Db	386	GNEGREFYMRQTGPISATLMTRPIKGPREIQLDLEMITVNTVINFRGSSVIRLRIYVSQ	445
Qy	421	YPF	423
Db	446	YPF	448

RESULT 11

ABU71315

ID ABU71315 standard; Protein; 448 AA.

XX

AC ABU71315;

XX

DT 10-JUN-2003 (first entry)

XX

DE Human PRO210 protein.

XX

KW Human; PRO; secreted; transmembrane; cytostatic; TNF-alpha; blood;
 KW tumour necrosis factor alpha release; chondrocyte cell; proliferation;
 KW differentiation; tumour; gene therapy.

XX

OS Homo sapiens.

XX

PN US2003036143-A1.

XX

PD 20-FEB-2003.

XX

PF 02-JUL-2002; 2002US-0187600.

XX

PR 16-SEP-1998; 98WO-US19330.

PR 07-OCT-1998; 98WO-US21141.

PR 01-DEC-1998; 98WO-US25108.

PR 08-MAR-1999; 99WO-US05028.

PR 14-MAY-1999; 99WO-US10733.

PR 02-JUN-1999; 99WO-US12252.

PR 01-SEP-1999; 99WO-US20111.

PR 15-SEP-1999; 99WO-US21090.

PR 01-DEC-1999; 99WO-US28301.

PR 02-DEC-1999; 99WO-US28551.

PR 30-DEC-1999; 99WO-US31274.

PR 05-JAN-2000; 2000WO-US00219.

PR 18-FEB-2000; 2000WO-US04341.

PR 18-FEB-2000; 2000WO-US04342.

PR 22-FEB-2000; 2000WO-US04414.
PR 24-FEB-2000; 2000WO-US05004.
PR 01-MAR-2000; 2000WO-US05601.
PR 02-MAR-2000; 2000WO-US05841.
PR 15-MAR-2000; 2000WO-US06884.
PR 30-MAR-2000; 2000WO-US08439.
PR 17-MAY-2000; 2000WO-US13705.
PR 22-MAY-2000; 2000WO-US14042.
PR 30-MAY-2000; 2000WO-US14941.
PR 02-JUN-2000; 2000WO-US15264.
PR 28-JUL-2000; 2000WO-US20710.
PR 24-AUG-2000; 2000WO-US23328.
PR 08-NOV-2000; 2000WO-US30952.
PR 01-DEC-2000; 2000WO-US32678.
PR 20-DEC-2000; 2000WO-US34956.
PR 28-FEB-2001; 2001WO-US06520.
PR 01-JUN-2001; 2001WO-US17800.
PR 20-JUN-2001; 2001WO-US19692.
PR 29-JUN-2001; 2001WO-US21066.
PR 09-JUL-2001; 2001WO-US21735.
PR 29-AUG-2001; 2001WO-US27099.
PR 18-SEP-1997; 97US-059263P.
PR 18-SEP-1997; 97US-059266P.
PR 17-OCT-1997; 97US-062250P.
PR 21-OCT-1997; 97US-063486P.
PR 24-OCT-1997; 97US-063120P.
PR 24-OCT-1997; 97US-063121P.
PR 28-OCT-1997; 97US-063540P.
PR 28-OCT-1997; 97US-063541P.
PR 28-OCT-1997; 97US-063544P.
PR 28-OCT-1997; 97US-063564P.
PR 29-OCT-1997; 97US-063734P.
PR 31-OCT-1997; 97US-063870P.
PR 31-OCT-1997; 97US-064103P.
PR 13-NOV-1997; 97US-065311P.
PR 21-NOV-1997; 97US-066120P.
PR 24-NOV-1997; 97US-066466P.
PR 24-NOV-1997; 97US-066772P.
PR 11-DEC-1997; 97US-069335P.
PR 12-DEC-1997; 97US-069425P.
PR 17-DEC-1997; 97US-069870P.
PR 18-DEC-1997; 97US-068017P.
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Db	26	QCTNGFDLDRQSGQCLDI	DECR	TI	PEACRGDMMC	CVNQNGGYLCI	PRTNPVYRGPYSNPYS	85
Qy	61	TPYSGPYPA	AAAPLSAPNYPTIS	RPLICRFGYQ	MDESNQCVDV	DECATDSHQCNPTQIC	ICI	120
Db	86	TPYSGPYPA	AAAPLSAPNYPTIS	RPLICRFGYQ	MDESNQCVDV	DECATDSHQCNPTQIC	ICI	145
Qy	121	NTEGGYTCSCTDGYWL	LEGQCLDI	DEC	RYGYCQQLCANV	PGSYSCTCNPGFTLN	EDGRSC	180
Db	146	NTEGGYTCSCTDGYWL	LEGQCLDI	DEC	RYGYCQQLCANV	PGSYSCTCNPGFTLN	EDGRSC	205
Qy	181	QDVNECATENPCVQTC	VNTYGSFICRCD	PGYELEEDGVH	CSDMDECSFSEFLC	QHECVNQ		240
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Qy	241	PGTYFCSCPPGYILL	DDNRSCQDINECE	HRNHTCNLQQTC	YNLQGGFKCIDPI	RCEEPYL		300
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Qy	301	RISDNRCMCPAENPG	CRDQPFTILYRDM	DVVS	GRSVPADIFQM	QATTRYPGAYYIFQ	IKS	360
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Db	446	YPF	448					

ABU72040

ID ABU72040 standard; Protein; 448 AA.

XX
AC ABU72040;

XX
DT 11-JUN-2003 (first entry)

XX
DE Novel human secreted and transmembrane protein PRO210.

XX
KW Human; secreted and transmembrane polypeptide; PRO;
KW fibroblast growth factor receptor; PRO533; PRO301; PRO187; PRO337;
KW PRO1411; PRO10096; PRO246; PRO6307; PRO6003; FGFR-3; FGFR-4; FGFR-1;
KW FGFR-2; PRO6004; PRO4356; PRO2630; PRO265; PRO951; bioactive molecule;
KW toxin; radiolabel; antibody; cell death; chromosome mapping;
KW gene mapping; transgenic animal; knockout animal; gene therapy;
KW tissue typing.

XX
OS Homo sapiens.

XX
PN US2002177165-A1.

XX
PD 28-NOV-2002.

PF 01-FEB-2002; 2002US-0066500.
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PR 14-JUL-1998; 98WO-US14552.
PR 10-SEP-1998; 98WO-US18824.
PR 14-SEP-1998; 98WO-US19093.
PR 16-SEP-1998; 98WO-US19330.
PR 17-SEP-1998; 98WO-US19437.
PR 20-NOV-1998; 98WO-US24855.
PR 25-NOV-1998; 98WO-US25190.
PR 01-DEC-1998; 98WO-US25108.
PR 08-MAR-1999; 99WO-US05028.
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PR 08-SEP-1999; 99WO-US20594.
PR 15-SEP-1999; 99WO-US21090.
PR 15-SEP-1999; 99WO-US21547.
PR 30-NOV-1999; 99WO-US28313.
PR 01-DEC-1999; 99WO-US28301.
PR 02-DEC-1999; 99WO-US28565.
PR 20-DEC-1999; 99WO-US30999.
PR 05-JAN-2000; 2000WO-US00219.
PR 18-FEB-2000; 2000WO-US04341.
PR 18-FEB-2000; 2000WO-US04342.
PR 22-FEB-2000; 2000WO-US04414.
PR 01-MAR-2000; 2000WO-US05601.
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PR 15-MAY-2000; 2000WO-US13358.
PR 17-MAY-2000; 2000WO-US13705.
PR 22-MAY-2000; 2000WO-US14042.
PR 30-MAY-2000; 2000WO-US14941.
PR 02-JUN-2000; 2000WO-US15264.
PR 11-AUG-2000; 2000WO-US22031.
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PR 24-AUG-2000; 2000WO-US23328.
PR 01-DEC-2000; 2000WO-US32678.
PR 28-FEB-2001; 2001WO-US06520.
PR 30-MAY-2001; 2001WO-US17443.
PR 01-JUN-2001; 2001WO-US17800.
PR 20-JUN-2001; 2001WO-US19692.
PR 29-JUN-2001; 2001WO-US21066.
PR 09-JUL-2001; 2001WO-US21735.
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PR 09-FEB-1998; 98US-074092P.
PR 25-MAR-1998; 98US-079294P.
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PR 17-AUG-1999; 99US-149396P.
PR 07-DEC-1999; 99US-169495P.
PR 15-NOV-2001; 2001US-0002796.

XX

PA (GETH) GENENTECH INC.

XX

PI Ashkenazi AJ, Baker KP, Botstein DA, Desnoyers L, Eaton DL;
PI Ferrara N, Fong S, Gao W, Gerber H, Gerritsen ME, Goddard A;
PI Godowski PJ, Gurney AL, Kljavin IJ, Mather JP, Napier MA, Pan J;
PI Paoni NF, Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PM;
PI Wood WI, Zhang Z;

XX

DR WPI; 2003-328482/31.

DR N-PSDB; ACA60458.

XX

PT Novel secreted and transmembrane polypeptide for modulating biological
PT activity of cell expressing the polypeptide, for identifying agonists
PT or antagonists of polypeptide, and as molecular weight markers -

XX

PS Claim 12; Fig 10; 254pp; English.

XX

CC The invention describes an isolated, secreted and transmembrane
CC polypeptide (PP), termed PRO PP or fibroblast growth factor receptor PP
CC (I). (I) is useful for detecting PRO533, PRO301, PRO187, PRO337,
CC PRO1411, PRO10096, PRO246, PRO6307, PRO6003, fibroblast growth factor
CC receptor (FGFR)-3, FGFR-4, FGFR-1, FGFR-2, PRO6004, PRO4356, PRO2630,
CC PRO265 or PRO951 polypeptide, and for linking a bioactive molecule to a
CC cell expressing the above polypeptides. The bioactive molecule, a toxin,
CC radiolabel or an antibody, causes cell death. PRO is useful in assays to
CC identify other proteins or molecules involved in binding interaction.
CC The polynucleotide (II) encoding (I) is useful in chromosome and gene
CC mapping, in generation of antisense RNA and DNA, for generating
CC transgenic animals or knockout animals which in turn are useful in the
CC development and screening of therapeutically useful reagents, to
CC construct hybridisation probes for mapping the gene which encodes the
CC PRO and for the genetic analysis of individuals with genetic disorders,
CC in gene therapy, for chromosome identification and as a chromosome
CC marker. (I) and (II) are useful for tissue typing. This is the amino
CC acid sequence of a novel human secreted and transmembrane PRO
CC polypeptide.

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SQ Sequence 448 AA;

Query Match 99.8%; Score 2401; DB 24; Length 448;
Best Local Similarity 99.8%; Pred. No. 3.2e-159;
Matches 422; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy    121 NTEGGYTCSC TDGYWLLEGQCLDIDECRYGYCQQLCANVPGSYSCTCNPGFTLNEDGRSC 180
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Qy    241 PGTYFCSCPPGYIILLDDNRSCQDINECEHRNHTCNLQQTTCYNLQGGFKCIDPIRCEEPYL 300
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Qy    301 RISDNRCMCPAENPGCRDQPFTILYRDMDVVSGRSVPADIFQMQATTRYPGAYYIFQIKS 360
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Qy    421 YPF 423
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Db    446 YPF 448
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RESULT 13

ABU65772

ID ABU65772 standard; Protein; 448 AA.

XX

AC ABU65772;

XX

DT 19-MAY-2003 (first entry)

XX

DE Human secreted/transmembrane protein, SEQ ID 408.

XX

KW Human; PRO; secreted protein; transmembrane protein;

KW cytostatic; antiarthritic; osteopathic; adrenal tumour; lung tumour;

KW colon tumour; breast tumour; prostate tumour; rectal tumour;

KW cervical tumour; liver tumour; TNF-alpha release; arthritis;

KW tumour necrosis factor alpha; chondrocyte cell; bone disorder;

KW cartilage disorder; sports injury.

XX

OS Homo sapiens.
XX
PN US2003036156-A1.
XX
PD 20-FEB-2003.
XX
PF 02-JUL-2002; 2002US-0188767.
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PR 16-SEP-1998; 98WO-US19330.
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PR	29-APR-1998;	98US-083559P.
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PR	06-MAY-1998;	98US-084414P.
PR	07-MAY-1998;	98US-084639P.
PR	07-MAY-1998;	98US-084640P.
PR	07-MAY-1998;	98US-084643P.
PR	15-MAY-1998;	98US-085579P.
PR	15-MAY-1998;	98US-085580P.
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PR	22-MAY-1998;	98US-086486P.
PR	28-MAY-1998;	98US-087098P.
PR	28-MAY-1998;	98US-087208P.
PR	02-JUN-1998;	98US-087609P.
PR	02-JUN-1998;	98US-087759P.
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PR	05-JUN-1998;	98US-088167P.
PR	05-JUN-1998;	98US-088202P.
PR	05-JUN-1998;	98US-088212P.
PR	05-JUN-1998;	98US-088217P.

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DT 28-MAY-2003 (first entry)

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KW cardiac insufficiency disorder; immune response; hearing loss;
KW auditory hair cell regeneration; bone disorder; cartilage disorder;
KW sports injury; arthritis.

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PN US2003032062-A1.

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XX

PA (GETH) GENENTECH INC.

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PI Ashkenazi AJ, Baker KP, Botstein DA, Desnoyers L, Eaton DL;

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43	351.5	14.6	2703	1	US-08-185-432-19	Sequence 19, Appl
44	351.5	14.6	2703	4	US-08-899-232-4	Sequence 4, Appli
45	350.5	14.6	652	2	US-08-751-305-2	Sequence 2, Appli

ALIGNMENTS

RESULT 1

US-08-884-072-1

; Sequence 1, Application US/08884072

; Patent No. 5872234

; GENERAL INFORMATION:

; APPLICANT: Bandman, Olga

; APPLICANT: Corley, Neil C.

; APPLICANT: Guegler, Karl J.

; TITLE OF INVENTION: HUMAN EXTRACELLULAR MATRIX PROTEINS

; NUMBER OF SEQUENCES: 6

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Incyte Pharmaceuticals, Inc.

; STREET: 3174 Porter Drive

; CITY: Palo Alto

; STATE: CA

; COUNTRY: USA

; ZIP: 94304

; COMPUTER READABLE FORM:

```

; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/884,072
; FILING DATE: Herewith
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0333 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; TELEX:
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 448 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: CORNNOT01
; CLONE: 45517
US-08-884-072-1

```

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Query Match          100.0%; Score 2407; DB 2; Length 448;
Best Local Similarity 100.0%; Pred. No. 1.7e-182;
Matches 423; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      1 QCTNGFDLDRQSGQCLDIDECRTIPEACRGDMMCVNQNGGYLCIPRTNPVYRGYPYNSNPYS 60
      |||
Db     26 QCTNGFDLDRQSGQCLDIDECRTIPEACRGDMMCVNQNGGYLCIPRTNPVYRGYPYNSNPYS 85

Qy     61 TPYSGPYPAAPPLSAPNYPTISRPLICRFGYQMDENQCVDVDECATDSHQCNPTQICI 120
      |||
Db     86 TPYSGPYPAAPPLSAPNYPTISRPLICRFGYQMDENQCVDVDECATDSHQCNPTQICI 145

Qy    121 NTEGGYTCSCTDGYWLLEGQCLDIDECRYGYCQQLCANVPGSYSCTCNPGFTLNEDGRSC 180
      |||
Db    146 NTEGGYTCSCTDGYWLLEGQCLDIDECRYGYCQQLCANVPGSYSCTCNPGFTLNEDGRSC 205

Qy    181 QDVNECATENPCVQTCVNTYGSFICRCDPGYELEEDGVHCSDMDECSFSEFLCQHECVNQ 240
      |||
Db    206 QDVNECATENPCVQTCVNTYGSFICRCDPGYELEEDGVHCSDMDECSFSEFLCQHECVNQ 265

Qy    241 PGTYFCSCPPGYILLDDNRSCQDINECEHRNHTCNLQQTTCYNLQGGFKCIDPIRCEEPYL 300
      |||
Db    266 PGTYFCSCPPGYILLDDNRSCQDINECEHRNHTCNLQQTTCYNLQGGFKCIDPIRCEEPYL 325

Qy    301 RISDNRCMCPAENPGCRDQPFTILYRDMDVVSGRSVPADIFQMQATTRYPGAYYIFQIKS 360
      |||
Db    326 RISDNRCMCPAENPGCRDQPFTILYRDMDVVSGRSVPADIFQMQATTRYPGAYYIFQIKS 385

```

Qy 361 GNEGREFYMRQTGPISATLVMTRPIKGPRIQLDLEMITVNTVINFRGSSVIRLRIYVSQ 420
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 386 GNEGREFYMRQTGPISATLVMTRPIKGPRIQLDLEMITVNTVINFRGSSVIRLRIYVSQ 445
 Qy 421 YPF 423
 |||
 Db 446 YPF 448

RESULT 2

US-09-212-168-1

; Sequence 1, Application US/09212168

; Patent No. 6303765

; GENERAL INFORMATION:

; APPLICANT: Bandman, Olga

; APPLICANT: Corley, Neil C.

; APPLICANT: Guegler, Karl J.

; TITLE OF INVENTION: HUMAN EXTRACELLULAR MATRIX PROTEINS

; NUMBER OF SEQUENCES: 6

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Incyte Pharmaceuticals, Inc.

; STREET: 3174 Porter Drive

; CITY: Palo Alto

; STATE: CA

; COUNTRY: USA

; ZIP: 94304

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette

; COMPUTER: IBM Compatible

; OPERATING SYSTEM: DOS

; SOFTWARE: FastSEQ for Windows Version 2.0

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/212,168

; FILING DATE:

; CLASSIFICATION:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/884,072

; FILING DATE:

; ATTORNEY/AGENT INFORMATION:

; NAME: Billings, Lucy J.

; REGISTRATION NUMBER: 36,749

; REFERENCE/DOCKET NUMBER: PF-0333 US

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 415-855-0555

; TELEFAX: 415-845-4166

; TELEX:

; INFORMATION FOR SEQ ID NO: 1:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 448 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; IMMEDIATE SOURCE:

; LIBRARY: CORNNOT01

; CLONE: 45517

US-09-212-168-1

Query Match 100.0%; Score 2407; DB 4; Length 448;
 Best Local Similarity 100.0%; Pred. No. 1.7e-182;
 Matches 423; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      1 QCTNGFDLDRQSGQCLDIDECRTIPEACRGDMMCVNQNGGYLCIPRTNPVYRGPYSNPYS 60
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      26 QCTNGFDLDRQSGQCLDIDECRTIPEACRGDMMCVNQNGGYLCIPRTNPVYRGPYSNPYS 85

Qy     61 TPYSGPYPAAPPLSAPNYPTISRPLICRFGYQMDESNQCDVDECATDSHQCNPTQICI 120
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     86 TPYSGPYPAAPPLSAPNYPTISRPLICRFGYQMDESNQCDVDECATDSHQCNPTQICI 145

Qy    121 NTEGGYTCSCTDGYWLLEGQCLDIDECRYGYCQQLCANVPGSYSCTCNPGFTLNEDGRSC 180
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    146 NTEGGYTCSCTDGYWLLEGQCLDIDECRYGYCQQLCANVPGSYSCTCNPGFTLNEDGRSC 205

Qy    181 QDVNECATENPCVQTCVNTYGSFICRCDPGYELEEDGVHCSDMDECSFSEFLCQHECVNQ 240
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    206 QDVNECATENPCVQTCVNTYGSFICRCDPGYELEEDGVHCSDMDECSFSEFLCQHECVNQ 265

Qy    241 PGTYFCSCPPGYILLDDNRSCQDINECEHRNHTCNLQOTCYNLQGGFKCIDPIRCEEPYL 300
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    266 PGTYFCSCPPGYILLDDNRSCQDINECEHRNHTCNLQOTCYNLQGGFKCIDPIRCEEPYL 325

Qy    301 RISDNRCMCPAENPGCRDQPFTILYRDMDVVSGRSVPADIFQMQATTRYPGAYYIFQIKS 360
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    326 RISDNRCMCPAENPGCRDQPFTILYRDMDVVSGRSVPADIFQMQATTRYPGAYYIFQIKS 385

Qy    361 GNEGREFYMRQTGPISATLVMTRPIKGPREIQLDLEMITVNTVINFRGSSVIRLRIYVSQ 420
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    386 GNEGREFYMRQTGPISATLVMTRPIKGPREIQLDLEMITVNTVINFRGSSVIRLRIYVSQ 445

Qy    421 YPF 423
      |||
Db    446 YPF 448
  
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RESULT 3
 US-09-312-283C-186
 ; Sequence 186, Application US/09312283C
 ; Patent No. 6573095
 ; GENERAL INFORMATION:
 ; APPLICANT: Watson, James D.
 ; APPLICANT: Strachan, Lorna
 ; APPLICANT: Sleeman, Matthew
 ; APPLICANT: Onrust, Rene
 ; APPLICANT: Murison, James G.
 ; APPLICANT: Kumble, Krishanand D.
 ; TITLE OF INVENTION: Compositions Isolated from Skin Cells
 ; TITLE OF INVENTION: and Methods for Their Use
 ; FILE REFERENCE: 11000.1011c2
 ; CURRENT APPLICATION NUMBER: US/09/312,283C
 ; CURRENT FILING DATE: 1999-05-14
 ; NUMBER OF SEQ ID NOS: 425
 ; SOFTWARE: FastSEQ for Windows Version 4.0
 ; SEQ ID NO 186

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;   LENGTH: 335
;   TYPE: PRT
;   ORGANISM: Mouse
US-09-312-283C-186
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Query Match 75.9%; Score 1827; DB 4; Length 335;
Best Local Similarity 95.2%; Pred. No. 7.8e-137;
Matches 319; Conservative 7; Mismatches 9; Indels 0; Gaps 0;

[illegible]

RESULT 4

US-09-188-930-186

; Sequence 186, Application US/09188930A

; Patent No. 6150502

; GENERAL INFORMATION:

; APPLICANT: Watson, James D.

; APPLICANT: Strachan, Lorna

; APPLICANT: Sleeman, Matthew

; APPLICANT: Onrust, Rene

; APPLICANT: Murison, James Greg

7 TITLE OF INVENTION: Compositions Isolated From Skin Cells

10 TITLE OF INVENTION: and Methods For Their Use

; FILE REFERENCE: 11000.1011c1

; CURRENT APPLICATION NUMBER: US/09/188,930A

; CURRENT FILING DATE: 1998-11-09

; NUMBER OF SEQ ID NOS: 348

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; SOFTWARE: FastSEQ for Windows Version 3.0
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; SEQ ID NO 186

; LENGTH: 337

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; TYPE: PRT
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; ORGANISM: Rat

; FEATURE:

; NAME/KEY: UNSURE

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; LOCATION: (14)...(124)
; NAME/KEY: UNSURE
; LOCATION: (135)...(135)
; NAME/KEY: UNSURE
; LOCATION: (141)...(141)
; NAME/KEY: UNSURE
; LOCATION: (166)...(166)
; NAME/KEY: UNSURE
; LOCATION: (167)...(167)
; NAME/KEY: UNSURE
; LOCATION: (183)...(183)
US-09-188-930-186

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Qy	89	RFGYQMDENQCVDVDDECATDSHQCNPTQICINTEGGYTCSCTDGYWLLLEGQCLDIDECR	148
Db	3	RFGYQMDENQCVDVDDECATDSHQCNPTQICINTEGGYTCSCTDGYWLLLEGQCLDIDECR	62
Qy	149	YGYCQQQLCANVPGSYSCTCNPGFTLNEDGRSCQDVNECATENPCVQTCVNTYGSFICRCD	208
Db	63	YGYCQQQLCANVPGSYSCTCNPGFTLNDDGRSCQDVNECETENPCVQTCVNTYGSFICRCD	122
Qy	209	PGYELEEDGVHCSMDDECSFSEFLCQHECVNQPGTYFCSCPPGYIILLDDNRSCQDINECE	268
Db	123	PXYELEEDGIHCXDMDECXFSEFLCQHECVNQPGSYFCSCPPGXLLLEDNRSCQDINECE	182
Qy	269	HRNHTCNLQQTCYNLQGGFKCIDPIRCEEPYLRI SDNRCMCPAENPGCRDQPFTILYRDM	328
Db	183	XRNHTCTPLQTCYNLQGGFKCIDPIVCEEPYLLIGDNRCMCPAENTGCRDQPFTILFRDM	242
Qy	329	DVVSGRSVPADIFQMQAATTRYPGAYYIFQIKSGNEGREFYMRQTGPISATLVMTRPIKGP	388
Db	243	DVVSGRSVPADIFQMQAATTRYPGAYYIFQIKSGNEGREFYMRQTGPISATLVMTRPIKGP	302
Qy	389	REIQLDLEMITVNTVINFRGSSVIRLRIYVSQYPF	423
Db	303	RDIQLDLEMITVNTVINFRGSSVIRLRIYVSOYPF	337


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;      ZIP: 20850
;      COMPUTER READABLE FORM:
;      MEDIUM TYPE: Floppy disk
;      COMPUTER: IBM PC compatible
;      OPERATING SYSTEM: PC-DOS/MS-DOS.
;      SOFTWARE: PatentIn Release #1.0, Version #1.30
;      CURRENT APPLICATION DATA:
;      APPLICATION NUMBER: US/08/833,963C
;      FILING DATE: 11-APR-1997
;      CLASSIFICATION: 435
;      PRIOR APPLICATION DATA:
;      APPLICATION NUMBER: WO PCT/US96/05033
;      FILING DATE: 10-APR-1996
;      ATTORNEY/AGENT INFORMATION:
;      NAME: Brookes, A. Anders
;      REGISTRATION NUMBER: 36,373
;      REFERENCE/DOCKET NUMBER: PF258
;      TELECOMMUNICATION INFORMATION:
;      TELEPHONE: 301-309-8504
;      TELEFAX: 301-309-8439
;      INFORMATION FOR SEQ ID NO: 2:
;      SEQUENCE CHARACTERISTICS:
;      LENGTH: 443 amino acids
;      TYPE: amino acid
;      TOPOLOGY: linear
;      MOLECULE TYPE: protein
US-08-833-963C-2

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Query Match          53.0%; Score 1276.5; DB 2; Length 443;
Best Local Similarity 52.0%; Pred. No. 3.1e-93;
Matches 220; Conservative 67; Mismatches 119; Indels 17; Gaps 4;

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Qy      1 QCTNGFDLDRQSGQCLDIDECRTIPEACRGDMMCVNQNGGYLCIPRTNPVYRGYPYNSNPYS 60
      :||:|::| | | |::|| |||||:|:| |:| |||||:|:| | :
Db      38 ECTDGYEWDPDSSQHCRDVNECLTIPEACKGEMKCINHYGGYLCIPRSAAVINDLHG---- 93

Qy      61 TPYSGPYPAAPPLSAPNYPTISRPLICRFGYQMDENQCVDVDECATDSHCNPTQICICI 120
      || | || || | | | | | | | | | | | | | | | | | | | | | | |
Db      94 ---EGP-PPVPVPAQHPN-----PCPPGYEPDDQDSCVDVDECAQALHDCRPSQDCH 141

Qy      121 NTEGGYTCSCTDGYWLLEGQCLDIDECRYGYCQQLCANVPGSYSCTCNPGFTLNEDGRSC 180
      | | | |:| || | : :|:||||||| || | | |:|:| | | | | | | | : |||
Db      142 NLPGSYQCTCPDGYRKIGPECVDIDECRYRYCQHRCVNLPGSFRCQCEPGFQLGPNNRSC 201

Qy      181 QDVNECATENPCVQTCVNTYGSFICRCDPGYELEEDGVHCSDMDECSFSEFLCQHECVNQ 240
      ||||| || | | |:|:|:|:| || | | | | | | | | | | | | | | |
Db      202 VDVNECDMGAPCEQRCFNSYGTFLCRCHQGYELHRDGFSCSDIDECSSYSSYLCQYRCVNE 261

Qy      241 PGTYFCSCPPGYILLDDNRSCQDINECEHRNHTCNLQQTTCYNLQGGFKCIDPIRCEEPYL 300
      || : | || | | | | | | | | | | | | | | | | | | | | | | | |
Db      262 PGRFSCHCPQGYQLL-ATRLCQDIDECESGAHQCEAQTCCVNFHGGYRCVDTNRCVEPYI 320

Qy      301 RISDNRCMCPAENPGCRDQPFITILYRDMDVVSGRSVPADIFQMQATTRYPGAYYIFQIKS 360
      :|:|:|:|:| | | | |:|:| | | : | | | | | | | | | | | | | | |
Db      321 QVSENRLCPASNPLCREQPSSIVHRYMTITERSVPADVFIQATSVYPGAYNAFQIRA 380

Qy      361 GNEGREFYMRQTGPISATLVMTRPIKGPREIQLDLEMITVNTVINFRGSSVIRLRIYVSQ 420

```

```

      || :||:| :|| ||: ||: |||| |||||:|:|:::| |||:| :|
Db      381 GNSQGDFYIRQINNVSAMLVLARPVTGPREYVLDLEMVTMNSLMSYRASSVLRLTVFVGA 440

QY      421 YPF 423
      ||
Db      441 YTF 443

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RESULT 6

US-08-980-514-1

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; Sequence 1, Application US/08980514
; Patent No. 6004753
; GENERAL INFORMATION:
; APPLICANT: Yue, Henry
; APPLICANT: Guegler, Karl J.
; APPLICANT: Shah, Purvi
; TITLE OF INVENTION: HUMAN S1-5-ECMP-LIKE PROT
; TITLE OF INVENTION: EIN
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Dr.
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/980,514
; FILING DATE: Filed Herewith
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0436 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-855-0555
; TELEFAX: 650-845-4166
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 443 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: BRSTNOT13
; CLONE: 2786449

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US-08-980-514-1

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Query Match          53.0%; Score 1276.5; DB 3; Length 443;
Best Local Similarity 52.0%; Pred. No. 3.1e-93;

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Matches 220; Conservative 67; Mismatches 119; Indels 17; Gaps 4;

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Qy      1 QCTNGFDLDRQSGQCLDIDECRTIPEACRGDMMCVNQNGGYLCIPRTNPVYRGPYSNPYS 60
      :||:|::| | | |::|| |||||:|:| |:| |||||:|:| | :
Db      38 ECTDGYEWDPSQHCRDVNECLTIPEACKGEMKCINHYGGYLCIPRSAAVINDLHG---- 93

Qy      61 TPYSGPYPAAPPLSAPNYPTISRPLICRFGYQMDENQCVDVDECATDSHQCNPQTQICI 120
      || | || || | | | | | | | | | | | | | | | | | | | | | | | |
Db      94 ---EGP-PPVPPAQHPN-----PCPPGYEPDDQDSCVDVDECAQALHDCRPSQDCH 141

Qy     121 NTEGGYTCSTDGWYLLLEGQCLDIDECRYGYCQQLCANVPGSYSCTCNPGFTLNEDGRSC 180
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db     142 NLPGSYQCTCPDGYRKIGPECVDIDECRYRYCQHRCVNLPGSFRCQCEPGFQLGPNNRSC 201

Qy     181 QDVNECATENPCVQTCVNTYGSFICRCDPGYELEEDGVHCSDMDECSFSEFLCQHECVNQ 240
      ||||| | | | | | | | | | | | | | | | | | | | | | | | | |
Db     202 VDVNECDMGAPCEQRCFNSYGTFLCRCHQGYELHRDGFSCSDIDECSSYSSYLCQYRCVNE 261

Qy     241 PGTYFCSCPPGYILLDDNRSCQDINECEHRNHTCNLQQTTCYNLQGGFKCIDPIRCEEPYL 300
      || : | | | | | | | | | | | | | | | | | | | | | | | | | |
Db     262 PGRFSCHCPQGYQLL-ATRLCQDIDECESGAHQCEAQTCVNFHGGYRCVDTNRCVEPYI 320

Qy     301 RISDNRCMCPAENPGCRDQPFTILYRDMDVVSGRSVPADIFQMQUATTRYPGAYYIFQIKS 360
      ::|:|:|:|:| | | | | | | | | | | | | | | | | | | | | |
Db     321 QVSENRLCPASNPLCREQPSSIVHRYMTITSERSVPADVFQIQATSVPYPGAYNAFQIRA 380

Qy     361 GNEGREFYMRQTGPISATLVMTRPIKGPREIQLDLEMITVNTVINFRGSSVIRLRIYVSQ 420
      || : | | | | : | | | | | | | | | | | | | | | | | | | |
Db     381 GNSQGDFYIRQINNVSAMLVLARPVTPGREYVLDLEMTMNSLMSYRASSVLRLTVFVGA 440

Qy     421 YPF 423
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Db     441 YTF 443

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RESULT 7

US-08-884-072-5

; Sequence 5, Application US/08884072

; Patent No. 5872234

; GENERAL INFORMATION:

; APPLICANT: Bandman, Olga

; APPLICANT: Corley, Neil C.

; APPLICANT: Guegler, Karl J.

; TITLE OF INVENTION: HUMAN EXTRACELLULAR MATRIX PROTEINS

; NUMBER OF SEQUENCES: 6

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Incyte Pharmaceuticals, Inc.

; STREET: 3174 Porter Drive

; CITY: Palo Alto

; STATE: CA

; COUNTRY: USA

; ZIP: 94304

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette

; COMPUTER: IBM Compatible

; OPERATING SYSTEM: DOS

; SOFTWARE: FastSEQ for Windows Version 2.0

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; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/884,072
; FILING DATE: Herewith
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0333 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; TELEX:
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 387 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GenBank
; CLONE: 458228
US-08-884-072-5

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Query Match          40.0%; Score 963.5; DB 2; Length 387;
Best Local Similarity 48.3%; Pred. No. 1.4e-68;
Matches 171; Conservative 55; Mismatches 123; Indels 5; Gaps 4;

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Qy      71 APPLSAPNYPTISRPLICRFGYQMDASNQCVDVDECATDSHCNPTQICINTEGGYTCSC 130
      | | | | : | | | : | | | | : | | | : | | | | : | | |
Db      38 ADPQRIPSNP--SHRIQCAAGYEQSEHNVCQDIDECTAGTHNCRADQVCINLRGSFACQC 95

Qy     131 TDGYWLLEGQCLDIDECRY-GYCQQLCANVPGSYSCNPGFTLNEDGRSCQDVNECATE 189
      | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      96 PPGYQKRGEQCVDIDECTIPPYCHQRCVNTPGSFYQCSPGFQLAANNYTCVDINECDAS 155

Qy     190 NPCVQTCVNTYGSFICRCDPGYELEEDGVHCSMDDECSFSEFLCQHECVNQPGTYFCSCP 249
      | | | | | | | | | | | | | | | | | | | | | | | | | |
Db     156 NQCAQQCYNILGSFICQCNQGYELSSDRLNCEDIDECRTSSYLCQYQCVNEPGKFSCMCP 215

Qy     250 PGYILLDDNRSCQDINECEHRNHTCNLQQTCYNLQGGFKCIDPIRCEEPYLRISDNRCMC 309
      | | : : : | | | | | | | | | | | | | | | | | | | | |
Db     216 QGYQVV-RSRTCQDINECETTNE-CREDEMCWNYHGGFRCYPRNPCQDPYILTPENRCVC 273

Qy     310 PAENPGCRDQPFTILYRDMDVVSGRSVPADIFQMQAATTRYPGAYYIFQIKSGNEGREFYM 369
      | | | | | | | | | | | | | | | | | | | | | | | | | |
Db     274 PVSNAMECRELPQSIVYKYSIRSDRSVPSDIFQIQATTIYANTINTFRIKSGNENGEFYL 333

Qy     370 RQTGPISATLVMTRPIKGPREIQLDLEMITVNTVINFRGSSVIRLRIYVSQYPF 423
      | | | | | | | | | | | | | | | | | | | | | | | | | |
Db     334 RQTSPVSAMLVLVKSLSGPREHIVDLEMLTVSSIGTFRFTSSVLRRLTIIVGPFSF 387

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RESULT 8
 US-08-833-963C-9

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; Sequence 9, Application US/08833963C
; Patent No. 5916769
; GENERAL INFORMATION:
;   APPLICANT: Olsen, et al.
;   TITLE OF INVENTION: Extracellular/Epidermal Growth Factor
;   TITLE OF INVENTION: HCABA58X
;   NUMBER OF SEQUENCES: 9
;   CORRESPONDENCE ADDRESS:
;     ADDRESSEE: Human Genome Sciences, Inc.
;     STREET: 9410 Key West Ave
;     CITY: Rockville
;     STATE: MD
;     COUNTRY: USA
;     ZIP: 20850
;   COMPUTER READABLE FORM:
;     MEDIUM TYPE: Floppy disk
;     COMPUTER: IBM PC compatible
;     OPERATING SYSTEM: PC-DOS/MS-DOS
;     SOFTWARE: PatentIn Release #1.0, Version #1.30
;   CURRENT APPLICATION DATA:
;     APPLICATION NUMBER: US/08/833,963C
;     FILING DATE: 11-APR-1997
;     CLASSIFICATION: 435
;   PRIOR APPLICATION DATA:
;     APPLICATION NUMBER: WO PCT/US96/05033
;     FILING DATE: 10-APR-1996
;   ATTORNEY/AGENT INFORMATION:
;     NAME: Brookes, A. Anders
;     REGISTRATION NUMBER: 36,373
;     REFERENCE/DOCKET NUMBER: PF258
;   TELECOMMUNICATION INFORMATION:
;     TELEPHONE: 301-309-8504
;     TELEFAX: 301-309-8439
;   INFORMATION FOR SEQ ID NO: 9:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH: 387 amino acids
;       TYPE: amino acid
;       STRANDEDNESS: single
;       TOPOLOGY: linear
;     MOLECULE TYPE: protein
US-08-833-963C-9

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Query Match          40.0%; Score 963.5; DB 2; Length 387;
Best Local Similarity 48.3%; Pred. No. 1.4e-68;
Matches 171; Conservative 55; Mismatches 123; Indels 5; Gaps 4;

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Qy      71 APPLSAPNYPTISRPLICRFGYQMDESNQCVDVDECATDSHQCNPQTQICINTEGGYTCSC 130
      | | | | : | | : | | : | | : | | : | | : | |
Db      38 ADPQRIPSNP--SHRIQCAAGYEQSEHNVCQDIDECTAGTHNCRADQVCINLRGSFACQC 95

Qy     131 TDGYWLLEGQCLDIDECRY-GYCQQLCANVPGSYSCTCNPGFTLNEDGRSCQDVNECATE 189
      | | | | | | | | | | | | | | | | | | | | : : | | : | |
Db     96 PPGYQKRGEQCVDIDECTIPPYCHQRCVNTPGSFYCQCSPGFQLAANNYTCVDINECDAS 155

Qy     190 NPCVQTCVNTYGSFICRCDPGYELEEDGVHCSMDDECSFSEFLCQHECVNQPGTYFCSCP 249
      | | | | | | | | | | : | | | | | : | | : | | : | | : | |
Db    156 NQCAQQCYNILGSFICQCNQGYELSSDRLNCEDIDECRTSSYLCQYQCVNEPGKFSCMCP 215

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; LIBRARY: GenBank
; CLONE: 458228
US-08-980-514-3

Query Match 40.0%; Score 963.5; DB 3; Length 387;
Best Local Similarity 48.3%; Pred. No. 1.4e-68;
Matches 171; Conservative 55; Mismatches 123; Indels 5; Gaps 4;

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Qy      71 APPLSAPNYPTISRPLICRFGYQMDESNCVDVDECATDSHQCNPQTQICINTEGGYTCSC 130
      | | | | : | | : | | : | | : | | : | | : | | : | |
Db      38 ADPQRIPSNP--SHRIQCAAGYEQSEHNVCQDIDECTAGTHNCRADQVCINLRGSFACQC 95

Qy     131 TDGYWLLEGQCLDIDECRY-GYCQQLCANVPGSYSCTCNPGFNEDGRSCQDVNECATE 189
      | | | | : | | | | | | | | : | | | | : | | | |
Db      96 PPGYQKRGEQCVDIDECTIPPYCHQRCVNTPGSFYQCSPGFQLAANNYTCVDINECDAS 155

Qy     190 NPCVQTCVNTYGSFICRCDPGYELEEDGVHCSDMDECSFSEFLCQHECVNQPPTYFCSCP 249
      | | | | | | | | : | | | | | | | : | | | | : | | | |
Db     156 NQCAQQCYNILGSFICQCNQGYELSSDRLNCEIDECRTSSYLCQYQCVNEPGKFSCMCP 215

Qy     250 PGYILLDDNRSCQDINECEHRNHTCNLQQTCYNLQGGFKCIDPIRCEEYPYLRISDNRCMC 309
      | | : : : | | | | | | | | | | : | | : | | : | | : | |
Db     216 QGYQVV-RSRTCQDINECETTNE-CREDEMWNHGGFRCYPRNPCQDPYILTPEINRCVC 273

Qy     310 PAENPGCRDQPFTILYRDMDVVSGRSVPADIFQMQATTRYPGAYYIFQIKSGNEGREFYM 369
      | | | | : | | : | | : | | | | : | | | | : | | | |
Db     274 PVSNAMECRELPQSIVYKYSIRSDRSVPSDIFQIQATTIYANTINTFRIKSGNENGEFY 333.

Qy     370 RQTGPISATLVMTRPIKGPRIQLDLEMITVNTVINFRGSSVIRLRIYVSQYPF 423
      | | | | : | | | | : : | | | | : | | | | : | | : |
Db     334 RQTSPVSAMLVLVKSLSGPREHIVDLEMLTVSSIGTFRTSSVLRLTIIVGPFSF 387
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RESULT 10

US-09-212-168-5

; Sequence 5, Application US/09212168

; Patent No. 6303765

; GENERAL INFORMATION:

; APPLICANT: Bandman, Olga

; APPLICANT: Corley, Neil C.

; APPLICANT: Guegler, Karl J.

; TITLE OF INVENTION: HUMAN EXTRACELLULAR MATRIX PROTEINS

; NUMBER OF SEQUENCES: 6

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Incyte Pharmaceuticals, Inc.

; STREET: 3174 Porter Drive

; CITY: Palo Alto

; STATE: CA

; COUNTRY: USA

; ZIP: 94304

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette

; COMPUTER: IBM Compatible

; OPERATING SYSTEM: DOS

; SOFTWARE: FastSEQ for Windows Version 2.0

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/212,168

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; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/884,072
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0333 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; TELEX:
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 387 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GenBank
; CLONE: 458228
US-09-212-168-5

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Query Match          40.0%; Score 963.5; DB 4; Length 387;
Best Local Similarity 48.3%; Pred. No. 1.4e-68;
Matches 171; Conservative 55; Mismatches 123; Indels 5; Gaps 4;

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Qy      71 APPLSAPNYPTISRPLICRFGYQMDESNQVDVDECATDSHCNPTQICINTEGGYTCSC 130
      | | | | : | | : | | | | : | | | | : | | | | : | | |
Db      38 ADPQRIPSNP--SHRIQCAAGYEQSEHNVCQDIDECTAGTHNCRADQVCINLRGSFACQC 95

Qy     131 TDGYWLLEGQCLDIDECRY-GYCQQLCANVPGSYSCNPGFTLNEDGRSCQDVNECATE 189
      | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      96 PPGYQKRGEQCVDIDECTIPPYCHQRCVNTPGSFYCQCSPGFQLAANNYTCDINECDAS 155

Qy     190 NPCVQTCVNTYGSFICRCDPGYELEEDGVHCSDMDECSFSEFLCQHECVNQPGETYFCSCP 249
      | | | | | | | | | | | | | | | | | | | | | | | | | |
Db     156 NQCAQQCYNILGSFICQCNQGYELSSDRLNCEDIDECRTSSYLCQYQCVNEPGKFSCMCP 215

Qy     250 PGYILLDDNRSCQDINECEHRNHTCNLQQTTCYNLQGGFKCIDPIRCEEYPYLRISDNRCMC 309
      | | : : : | | | | | | | | | | | | | | | | | | | | |
Db     216 QGYQVV-RSRTCQDINECETTNE-CREDEMCWNYHGGFRCYPRNPCQDPYILTPENRCVC 273

Qy     310 PAENPGCRDQPFTILYRDMDVVSGRSVPADIFQMQATTRYPGAYYIFQIKSGNEGREFYM 369
      | | | | : | | : | | : | | | | | | | | | | | | | | | |
Db     274 PVSNAMECRELPQSIVYKYSIRSRSVPSDIFQIQATTIYANTINTFRIKSGNENGFEFYL 333

Qy     370 RQTGPISATLVMTRPIKGPREIQLDLEMITVNTVINFRGSSVIRLRIYVSQYPF 423
      | | | | : | | | | : : | | | | : | | | | : | | | | : | |
Db     334 RQTSPVSAMLVLVKSLSGPREHIVDLEMLTVSSIGTFRTSSVLRLLTIIVGPFSS 387

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```

RESULT 11
US-09-188-930-336
; Sequence 336, Application US/09188930A
; Patent No. 6150502

```



```
; GENERAL INFORMATION:
; APPLICANT: Watson, James D.
; APPLICANT: Strachan, Lorna
; APPLICANT: Sleeman, Matthew
; APPLICANT: Onrust, Rene
; APPLICANT: Murison, James Greg
; TITLE OF INVENTION: Compositions Isolated From Skin Cells
; TITLE OF INVENTION: and Methods For Their Use
; FILE REFERENCE: 11000.1011c1
; CURRENT APPLICATION NUMBER: US/09/188,930A
; CURRENT FILING DATE: 1998-11-09
; NUMBER OF SEQ ID NOS: 348
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 336
; LENGTH: 274
; TYPE: PRT
; ORGANISM: Human
US-09-188-930-336
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Query Match          37.9%; Score 912.5; DB 3; Length 274;
Best Local Similarity 56.0%; Pred. No. 1e-64;
Matches 154; Conservative 47; Mismatches 73; Indels 1; Gaps 1;
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Qy      149 YGYCQQLCANVPGSYSCTCNPGFTLNEDGRSCQDVNECATENPCVQTCVNTYGSFICRCD 208
      | | | | | | : | | | | | : | | | | | | | | | | | | | | | | | |
Db      1 YRYCQHRCVNLPGSFRCQCEPGFQLGPNRNSCVDVNECDMGAPCEQRCFNSYGTFLCRCH 60

Qy      209 PGYELEEDGVHCSMDDECSFSEFLCQHECVNQPGTYFCSCPPGYILLDDNRSCQDINECE 268
      | | | | | | | | | | | | : | | | | | | | | | | | | | | | | |
Db      61 QGYELHRDGFSCSDIDECSYSSYLCQYRCVNEPGRFSCHCPQGYQLL-ATRLCQDIDECE 119

Qy      269 HRNHTCNLQQTTCYNLQGGFKCIDPIRCEEPYLRISDNRCMCPAENPGCRDQPFTILYRDM 328
      | | : | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      120 SGAHQCSEAQTCVNFHGGYRCVDTNRCVEPYIQVSENRCLCPASNPLCREQPSSIVHRYM 179

Qy      329 DVVSGRSVPADIFQMQAATTRYPGAYYIFQIKSGNEGREFYMRQTGPISATLVMTRPIKGP 388
      : | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      180 TITSERVSPADVFIQATSVPYAGYNAFQIRAGNSQGDFYIRQINNVSAMLVLARPVTPG 239

Qy      389 REIQLDLEMITVNTVINFRGSSVIRLRIYVSQYPF 423
      | | | | | | | | | | | | | | | | | | | | | | | |
Db      240 REYVLDLEMTMNSLMSYRASSVLRLTVFVGAYTF 274
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RESULT 12

US-09-312-283C-336

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; Sequence 336, Application US/09312283C
; Patent No. 6573095
; GENERAL INFORMATION:
; APPLICANT: Watson, James D.
; APPLICANT: Strachan, Lorna
; APPLICANT: Sleeman, Matthew
; APPLICANT: Onrust, Rene
; APPLICANT: Murison, James G.
; APPLICANT: Kumble, Krishanand D.
; TITLE OF INVENTION: Compositions Isolated from Skin Cells
; TITLE OF INVENTION: and Methods for Their Use
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; FILE REFERENCE: 11000.1011c2
; CURRENT APPLICATION NUMBER: US/09/312,283C
; CURRENT FILING DATE: 1999-05-14
; NUMBER OF SEQ ID NOS: 425
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 336
; LENGTH: 274
; TYPE: PRT
; ORGANISM: Mouse
US-09-312-283C-336

Query Match 37.9%; Score 912.5; DB 4; Length 274;
Best Local Similarity 56.0%; Pred. No. 1e-64;
Matches 154; Conservative 47; Mismatches 73; Indels 1; Gaps 1;

Qy 149 YGYCQQLCANVPGSYSCTCNPGFTLNEDGRSCQDVNECATENPCVQTCVNTYGSFICRCD 208
| ||| | :|||: | | ||| | : ||| |||| | | | | :|||:| |||
Db 1 YRYCQHRCVNLPGSFRCQCEPGFQLGPNNRSCVDVNECDMGAPCEQRCFNSYGTFLCRCH 60

Qy 209 PGYELEEDGVHCSMDDECSFSEFLCQHECVNQPGTYFCSCPPGYILLDDNRSCQDINECE 268
||| | | |||:||||:| :|||: |||:| | : | | | | | | | | |||:| |||
Db 61 QGYELHRDGFSCSDIDECSSYSSYLCQYRCVNEPGRFSCHCPQGYQLL-ATRLCQDIDECE 119

Qy 269 HRNHTCNLQQTTCYNLQGGFKCIDPIRCEEPYLRISDNRCMCPAENPGCRDQPFTILYRDM 328
| : | || | | |||:|:| | | |||:|:| |||:| || | | | | | | | | :|:| | |
Db 120 SGAHQCSAQTCVNFHGGYRCVDTNRCVEPYIQVSENRLCPASNPLCREQPSSIVHRYM 179

Qy 329 DVVSGRSVPADIFQMQATTRYPGAYYIFQIKSGNEGREFYMRQTGPISATLVMTRPIKGP 388
: | |||||:|:|:|:| |||| | |||:| | :||| | :| | | :| | |
Db 180 TITSERVSPADVFIQATSVPYPGAYNAFQIRAGNSQGDFYIRQINNVSAMLVLARPVTPG 239

Qy 389 REIQLDLEMITVNTVINFRGSSVIRLRIYVSQYPF 423
| | |||||:|:|:|:| |||:| | :| | | |
Db 240 REYVLDLEMVTMNSLSYRASSVLRLTVFVGAYTF 274

RESULT 13

5177197-30

;Patent No. 5177197

; APPLICANT: KANZAKI, TETSUTO;OLOFSSON, ANDERS;MOREN, ANITA;
;WERNSTEDT, CHRISTER;HELLMAN, ULF;MIYAZONO, KOHEI;CLAESSON-WELSH,
;LENA;HELDIN, CARL-HENRIK

; TITLE OF INVENTION: ISOLATED NUCLEOTIDE SEQUENCE EXPRESSING
;HUMAN TRANSFORMING GROWTH FACTOR-BETA1-BINDING PROTEIN

; NUMBER OF SEQUENCES: 53

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/07/487,343

; FILING DATE: 27-FEB-1990

;SEQ ID NO:30:

; LENGTH: 1394

5177197-30

Query Match 22.4%; Score 539; DB 6; Length 1394;
Best Local Similarity 29.6%; Pred. No. 1.9e-34;
Matches 126; Conservative 51; Mismatches 126; Indels 122; Gaps 17;

Qy 2 CTNGFDLDRQSGQCLDIDECRTIPEACRGDMMCVNQNGGYLCIPRTNPVYRGPYSNPYST 61

Db	573	CYEGYRFSEQQRKCVDI	DECTQVQHLC-SQGR	CENTEGSFLCI-----	614
Qy	62	PYSGPYPAAPPLSAPNYPTISRPLI-----	CRFGYQMDES	NQCVDVD	104
Db	615	-CPAGFMASEEGTNCIDVDECLRPDVC	GEGHCVNTVGA	FRCEYCD	SGYRMTQGRCEDID 673
Qy	105	ECATDSHQCNPTQICINTEGGYTC-SCTDGYWLLEGQCLDI	DEC-RYGYCQQ-LCANVPG	161	
Db	674	ECLNPS-TC-PDEQCVNSPGSYQCV	PCTEGFRGWNGQCLDVDECLEPNVCANGDCSNLEG	731	
Qy	162	SYSCTCNPGFTLNEDGRSCQDVNECATENPCVQ-----	194		
Db	732	SYMCSCHKGYTRTPDHKHC	RDIDECQQGNLCVNGQCKNTEGSFRCTCGQGYQLSAAKDQC	791	
Qy	195	-----TCVNTYGSFICRCDPGYELEEDGVHCS	DMDECSFSEFLCQH-ECV	238	
Db	792	EDIDECQHRHLCAHGQCRNTEGSFQCVCDQGYRASGLGDH	CEDINECLEDKSVCQRGDCI	851	
Qy	239	NQPGTYFCSCPPGYILLDDNRSCQDINECEHRNHTCNLQQT	CYNLQGGFKCI-----	290	
Db	852	NTAGSYDCTCPDGF-QLDDNKTCQDINECEHPG-LCGPQGECLNTEGSFHCVCQ	QGFSSIS	909	
Qy	291	-DPIRCEEPYLRIS-----DN-----RCMC-----PAENPGCRDQ	PFTILYRDM	328	
Db	910	ADGRTCEDIDECVNNTVCD	SHGFCDNTAGSFRCLCYQGFQAPQDGQGCVD-----VNEC	963	
Qy	329	DVVS	G 333		
Db	964	ELLSG	968		

RESULT 14

US-09-482-273-159

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; Sequence 159, Application US/09482273
; Patent No. 6534631
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 71 Human Secreted Proteins
; FILE REFERENCE: PZ030P1
; CURRENT APPLICATION NUMBER: US/09/482,273
; CURRENT FILING DATE: 2000-01-13
; EARLIER APPLICATION NUMBER: PCT/US99/15849
; EARLIER FILING DATE: 1999-07-14
; EARLIER APPLICATION NUMBER: 60/092,921
; EARLIER FILING DATE: 1998-07-15
; EARLIER APPLICATION NUMBER: 60/092,922
; EARLIER FILING DATE: 1998-07-15
; EARLIER APPLICATION NUMBER: 60/092,956
; EARLIER FILING DATE: 1998-07-15
; NUMBER OF SEQ ID NOS: 267
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 159
; LENGTH: 575
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-482-273-159

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Query Match 21.5%; Score 518; DB 4; Length 575;
 Best Local Similarity 29.5%; Pred. No. 3.2e-33;
 Matches 140; Conservative 56; Mismatches 157; Indels 122; Gaps 20;

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Qy      2 CTNGFDLDRQSGQCLDIDECRTIPEACRGDMMCVNQNGGYLCIPRTNPVYRGPYSNPYST 61
      | | | : | | | : | : | | | | | | | | | | | | | | | |
Db      170 CPEGFELDSQGAFCVDVDECAWDAHLCREGQRCVNLLGSYRCLPDCGP----- 217

Qy      62 PYSGPYPAAPPLSAPNYPTISRPLICRFGYQMDENQCVDVDECATDSHCNPTQICIN 121
      | | | : | | | : | : | | | | | | | | | | | | | | | |
Db      218 -----GFRVADGAGCEDVDECLEGLDDCHYNQLCEN 248

Qy     122 TEGGYTCSTDGWLLLEG---QCLDIDECRY--GYCQQLCANVPGSYSCTCNPGFTLNE 176
      | | | : | | | : | : | | | | | | | | | | | | | | | |
Db     249 TPGGHRCSCPRGY-RMQGPSLPCLDVNECLQLPKACAYQCHNLQGSYRCLCPPGQTLLRD 307

Qy     177 GRSC-----QDVNECATENPCV-----QTCVNTYGSFI-----CRCD 208
      | : | | | : | : | : | : | : | : | : | : | : | : |
Db     308 GKACTSLERNQNVTTVSHRGPLLPLWRPWSIPGTSYHAWVSLRPGPMALSSVGRWCP 367

Qy     209 PGYELEEDGVHCSDMDECSFSEFLCQHECVNQPGTYFCSCPPGYILLDDNRSCQDINECE 268
      | | : : : | | : | : | | | | | | | | | | | | | | | |
Db     368 PGF-IRQNGV-CTDLDECRVRN-LCQHACRNTEGSYQCLCPAGYRLLPSGKNCQDINECE 424

Qy     269 HRNHTCNLQQTCYNLQGGFKCIDPIRCEEPYLRISDNRCMCPA-----ENPG-----CRD 318
      : | | | | : | : | : | : | | | | | | | | | | | |
Db     425 EESIECGPGQMCFNTRGSYQCVD-----TPCPATYRQGPSPGTCFRRCSQ 469

Qy     319 Q-----PFTILYRDMDVVSGRSVPADIFQMQATTR--YPGAYYIFQIKSGNEGREFYMRQ 371
      | | : | | : : | | : : | : | | | : : | : | | | |
Db     470 DCGTGGPSTLQYRLLPLPLGVRAHHDVARLTAFAFSEVGV PANRTELSMLEPDPRSPFALR- 528

Qy     372 TGPISATL--VMTRPIKGPRIE-QLDLEMITVNTVINFRGSSVIRLRIYVSQYPF 423
      | : | | | | | | | : : | : | | | | | | | | | |
Db     529 --PLRAGLGAVYTR-----RALTRAGLYRLTVRAAAP-RHQSVFVLLIAVSPYPY 575
  
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RESULT 15

US-09-482-273-245

; Sequence 245, Application US/09482273

; Patent No. 6534631

; GENERAL INFORMATION:

; APPLICANT: Rosen et al.

; TITLE OF INVENTION: 71 Human Secreted Proteins

; FILE REFERENCE: PZ030P1

; CURRENT APPLICATION NUMBER: US/09/482,273

; CURRENT FILING DATE: 2000-01-13

; EARLIER APPLICATION NUMBER: PCT/US99/15849

; EARLIER FILING DATE: 1999-07-14

; EARLIER APPLICATION NUMBER: 60/092,921

; EARLIER FILING DATE: 1998-07-15

; EARLIER APPLICATION NUMBER: 60/092,922

; EARLIER FILING DATE: 1998-07-15

; EARLIER APPLICATION NUMBER: 60/092,956

; EARLIER FILING DATE: 1998-07-15

; NUMBER OF SEQ ID NOS: 267

; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 245
; LENGTH: 638
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-482-273-245

Query Match 21.5%; Score 518; DB 4; Length 638;
Best Local Similarity 29.5%; Pred. No. 3.6e-33;
Matches 140; Conservative 56; Mismatches 157; Indels 122; Gaps 20;

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Qy      2 CTNGFDLDRQSGQCLDIDECRTIPEACRGDMMCVNQNGGYLCIPRTNPVYRGPYSNPYST 61
      | | | : | | | : | : | | | | | | | | | | | | | | | |
Db      233 CPEGFELDSQGAFCVDVDECAWDAHLCREGQRCVNLLGSYRCLPDCGP----- 280

Qy      62 PYSGPYPAAAPPLSAPNYPTISRPLICRFGYQMDENQCVDVDECATDSHCNPTQICIN 121
      | | | : | | | : | : | | | | | | | | | | | | | | | |
Db      281 -----GFRVADGAGCEDVDECLEGLDDCHYNQLCEN 311

Qy     122 TEGGYTCSDTDGYWLLEG---QCLDIDECRY--GYCQQLCANVPGSYSCTCNPGFTLNED 176
      | | | : | | | : | : | | | : | | | | | | | | | | | |
Db     312 TPGGHRCS CPRGY-RMQGPSLPCLDVNECLQLPKACAYQCHNLQGSYRCLCPPGQTLLRD 370

Qy     177 GRSC-----QDVNECATENPCV-----QTCVNTYGSFI-----CRCD 208
      | : | | | : | : | : | : | : | : | : | : | : | : |
Db     371 GKACTSLERNQNVTTVSHRGPLLPWLRPWASIPGTSYHAWVSLRPGPMALSSVGRWCP 430

Qy     209 PGYELEEDGVHCSMDDECSFSEFLCQHECVNQPGTYFCSCPPGYILLDDNRSCQDINECE 268
      | | : : : | | | : | : | | | | | | | | | | | | | | |
Db     431 PGF-IRQNGV-CTDLDECRVRN-LCQHACRNTEGSYQCLCPAGYRLLPSGKNCQDINECE 487

Qy     269 HRNHTCNLQQTCYNLQGGFKCIDPIRCEEPYLRISDNRCMCPA-----ENPG-----CRD 318
      : | | | | : | : | : | : | | | | | | | | | | | |
Db     488 EESIECGPGQMCFNTRGSYQCVD-----TPCPATYRQGPSPGTCFRRC SQ 532

Qy     319 Q-----PFTILYRDMDVVSGRSVPADIFQM QATTR--YPGAYYIFQIKSGNEGREFYMRQ 371
      | | : | | : : | | | : : | : | | | : : | : | | |
Db     533 DCGTGGPSTLQYRLLPLPLGVRAHHDVARLTAFSEVGVPANRTELSMLEPDPRSPFALR- 591

Qy     372 TGPI SATL--VMTRPIKGPRI-QLDLEMITVNTVINFRGSSVIRLRIYVSQYPF 423
      | : | | | | | | : : | : | | | | | | | | | |
Db     592 --PLRAGLGAVYTR-----RALTRAGLYRLTVRAAAP-RHQSVFVLLIAVSPYPY 638
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Search completed: January 9, 2004, 12:35:36
Job time : 16.0551 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: January 9, 2004, 12:34:12 ; Search time 28.1676 Seconds
(without alignments)
3026.121 Million cell updates/sec

Title: US-09-674-379A-14
Perfect score: 2407
Sequence: 1 QCTNGFDLDRQSGQCLDIDE.....INFRGSSVIRLRIYVSQYPF 423

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 747907 seqs, 201509753 residues

Total number of hits satisfying chosen parameters: 747907

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications_AA:*

- 1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
- 2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
- 3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
- 4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*
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- 8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
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- 11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep:*
- 12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep:*
- 13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep:*
- 14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*
- 15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep:*
- 16: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
- 17: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep:*
- 18: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	%	Query				
No.	Score	Match Length	DB	ID		Description

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2	2407	100.0	448	9	US-09-275-805-2	Sequence 2, Appli
3	2407	100.0	448	9	US-09-836-561-1	Sequence 1, Appli
4	2407	100.0	448	14	US-10-041-016-2	Sequence 2, Appli
5	2401	99.8	448	12	US-10-199-672-408	Sequence 408, App
6	2401	99.8	448	12	US-10-187-749-408	Sequence 408, App
7	2401	99.8	448	12	US-10-194-457-408	Sequence 408, App
8	2401	99.8	448	12	US-10-184-642-408	Sequence 408, App
9	2401	99.8	448	12	US-10-196-747-408	Sequence 408, App
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ALIGNMENTS

RESULT 1

US-09-083-002-2

; Sequence 2, Application US/09083002

; Patent No. US20010016650A1

; GENERAL INFORMATION:

; APPLICANT: Jacobs, Kenneth

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; APPLICANT: McCoy, John M.
; APPLICANT: Racie, Lisa A.
; APPLICANT: LaVallie, Edward R.
; APPLICANT: Merberg, David
; APPLICANT: Treacy, Maurice
; APPLICANT: Evans, Cheryl
; APPLICANT: Agostino, Michael
; APPLICANT: Lu, Zhijian
; APPLICANT: Honjo, Tasuku
; APPLICANT: Tashiro, Kei
; APPLICANT: Nakamura, Tomoyuki
; TITLE OF INVENTION: SECRETED PROTEINS
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genetics Institute, Inc.
; STREET: 87 CambridgePark Drive
; CITY: Cambridge
; STATE: MA
; COUNTRY: U.S.A.
; ZIP: 02140
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/083,002
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Sprunger, Suzanne A.
; REGISTRATION NUMBER: P-41,323
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 498-8284
; TELEFAX: (617) 876-5851
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 448 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-083-002-2

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Query Match          100.0%;  Score 2407;  DB 9;  Length 448;
Best Local Similarity 100.0%;  Pred. No. 3.3e-183;
Matches 423;  Conservative 0;  Mismatches 0;  Indels 0;  Gaps 0;

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RESULT 2

US-09-275-805-2

; Sequence 2, Application US/09275805

; Patent No. US20010051358A1

; GENERAL INFORMATION:

; APPLICANT: OLSEN, HENRIK S.

; APPLICANT: LI, HAODONG

; TITLE OF INVENTION: EXTRACELLULAR EPIDERMAL GROWTH FACTOR

; TITLE OF INVENTION: LIKE PROTEIN

; NUMBER OF SEQUENCES: 11

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: HUMAN GENOME SCIENCES, INC.

; STREET: 9410 KEY WEST AVENUE

; CITY: ROCKVILLE

; STATE: MD

; COUNTRY: US

; ZIP: 20850

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/275,805

; FILING DATE:

; CLASSIFICATION:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/839,525

; FILING DATE:

; ATTORNEY/AGENT INFORMATION:

; NAME: BROOKES, ANDERS A.

; REGISTRATION NUMBER: 36,373

; REFERENCE/DOCKET NUMBER: PF224

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; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 309-8509
; TELEFAX: (301) 309-8512
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 448 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-275-805-2

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Query Match          100.0%; Score 2407; DB 9; Length 448;
Best Local Similarity 100.0%; Pred. No. 3.3e-183;
Matches 423; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 3

US-09-836-561-1

; Sequence 1, Application US/09836561

; Patent No. US20020038006A1

GENERAL INFORMATION:

; APPLICANT: Bandman, Olga

; Corley, Neil C.

; Guegler, Karl J.

; TITLE OF INVENTION: HUMAN EXTRACELLULAR MATRIX PROTEINS

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;      NUMBER OF SEQUENCES: 6
;      CORRESPONDENCE ADDRESS:
;          ADDRESSEE: Incyte Pharmaceuticals, Inc.
;          STREET: 3174 Porter Drive
;          CITY: Palo Alto
;          STATE: CA
;          COUNTRY: USA
;          ZIP: 94304
;      COMPUTER READABLE FORM:
;          MEDIUM TYPE: Diskette
;          COMPUTER: IBM Compatible
;          OPERATING SYSTEM: DOS
;          SOFTWARE: FastSEQ for Windows Version 2.0
;      CURRENT APPLICATION DATA:
;          APPLICATION NUMBER: US/09/836,561
;          FILING DATE: 16-Apr-2001
;          CLASSIFICATION: <Unknown>
;      PRIOR APPLICATION DATA:
;          APPLICATION NUMBER: 09/212,168
;          FILING DATE: <Unknown>
;      ATTORNEY/AGENT INFORMATION:
;          NAME: Billings, Lucy J.
;          REGISTRATION NUMBER: 36,749
;          REFERENCE/DOCKET NUMBER: PF-0333 US
;      TELECOMMUNICATION INFORMATION:
;          TELEPHONE: 415-855-0555
;          TELEFAX: 415-845-4166
;          TELEX: <Unknown>
;      INFORMATION FOR SEQ ID NO: 1:
;          SEQUENCE CHARACTERISTICS:
;              LENGTH: 448 amino acids
;              TYPE: amino acid
;              STRANDEDNESS: single
;              TOPOLOGY: linear
;          IMMEDIATE SOURCE:
;              LIBRARY: CORNNOT01
;              CLONE: 45517
;          SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-836-561-1

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Query Match          100.0%;  Score 2407;  DB 9;  Length 448;
Best Local Similarity 100.0%;  Pred. No. 3.3e-183;
Matches 423;  Conservative 0;  Mismatches 0;  Indels 0;  Gaps 0;

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Qy    121 NTEGGYTCSC TDGYWLLEGQCLDIDECRYGYCQQQLCANVPGSYSCTCNP GFTLNEDGRSC 180
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Db    146 NTEGGYTCSC TDGYWLLEGQCLDIDECRYGYCQQQLCANVPGSYSCTCNP GFTLNEDGRSC 205

Qy    181 QDVNECATENPCVQTCVNTYGSFICRCDPGYELEEDGVHCSMDDECSFSEFLCQHECVNQ 240

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RESULT 4

US-10-041-016-2

; Sequence 2, Application US/10041016

; Publication No. US20020165151A1

; GENERAL INFORMATION:

; APPLICANT: Jacobs, Kenneth
; McCoy, John M.
; Racie, Lisa A.
; LaVallie, Edward R.
; Merberg, David
; Treacy, Maurice
; Evans, Cheryl
; Agostino, Michael
; Lu, Zhijian
; Honjo, Tasuku

; TITLE OF INVENTION: SECRETED PROTEINS

; NUMBER OF SEQUENCES: 2

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Genetics Institute, Inc.
; STREET: 87 CambridgePark Drive
; CITY: Cambridge
; STATE: MA
; COUNTRY: U.S.A.
; ZIP: 02140

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/10/041,016
; FILING DATE: 07-Jan-2002
; CLASSIFICATION: <Unknown>

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US/09/083,002
; FILING DATE: 21-MAR-1998

; ATTORNEY/AGENT INFORMATION:

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;          NAME: Sprunger, Suzanne A.
;          REGISTRATION NUMBER: P-41,323
;          TELECOMMUNICATION INFORMATION:
;          TELEPHONE: (617) 498-8284
;          TELEFAX: (617) 876-5851
;          INFORMATION FOR SEQ ID NO: 2:
;          SEQUENCE CHARACTERISTICS:
;          LENGTH: 448 amino acids
;          TYPE: amino acid
;          STRANDEDNESS: No. US20020165151A1 Relevant
;          TOPOLOGY: linear
;          MOLECULE TYPE: protein
;          SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-10-041-016-2

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Query Match          100.0%; Score 2407; DB 14; Length 448;
Best Local Similarity 100.0%; Pred. No. 3.3e-183;
Matches 423; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db      26 QCTNGFDLDRQSGQCLDIDECRTIPEACRGDMMCVNQNGGYLCIPRTNPVYRGYPYSNPYS 85

Qy      61 TPYSGPYPAAPPLSAPNYPTISRPLICRFGYQMDESNQCVDVDECATDSHQCNPTQICI 120
      |||
Db      86 TPYSGPYPAAPPLSAPNYPTISRPLICRFGYQMDESNQCVDVDECATDSHQCNPTQICI 145

Qy     121 NTEGGYTCSTDGWYLLLEGQCLDIDECRYGYCQQLCANVPGSYSCTCNPGFTLNEDGRSC 180
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Db     146 NTEGGYTCSTDGWYLLLEGQCLDIDECRYGYCQQLCANVPGSYSCTCNPGFTLNEDGRSC 205

Qy     181 QDVNECATENPCVQTCVNTYGSFICRCDPGYELEEDGVHCSDMDECSFSEFLCQHECVNQ 240
      |||
Db     206 QDVNECATENPCVQTCVNTYGSFICRCDPGYELEEDGVHCSDMDECSFSEFLCQHECVNQ 265

Qy     241 PGTYFCSCPPGYILLDDNRSCQDINECEHRNHTCNLQQTTCYNLQGGFKCIDPIRCEEPYL 300
      |||
Db     266 PGTYFCSCPPGYILLDDNRSCQDINECEHRNHTCNLQQTTCYNLQGGFKCIDPIRCEEPYL 325

Qy     301 RISDNRCMCPAENPGCRDQPFTILYRDMDVVSGRSVPADIFQMQATTRYPGAYYIFQIKS 360
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Db     326 RISDNRCMCPAENPGCRDQPFTILYRDMDVVSGRSVPADIFQMQATTRYPGAYYIFQIKS 385

Qy     361 GNEGREFYMRQTGPISATLVMTRPIKGPRIQLDLEMITVNTVINFRGSSVIRLRIYVSQ 420
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Db     386 GNEGREFYMRQTGPISATLVMTRPIKGPRIQLDLEMITVNTVINFRGSSVIRLRIYVSQ 445

Qy     421 YPF 423
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Db     446 YPF 448

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RESULT 5

US-10-199-672-408

; Sequence 408, Application US/10199672

; Publication No. US20030148442A1

; GENERAL INFORMATION:

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; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3430R1C1
; CURRENT APPLICATION NUMBER: US/10/199,672
; CURRENT FILING DATE: 2002-07-18
; PRIOR APPLICATION NUMBER: US/10/052,586
; PRIOR FILING DATE: 2002-01-15
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059266
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063120
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063121
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063486
; PRIOR FILING DATE: 1997-10-21
; PRIOR APPLICATION NUMBER: 60/063540
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063541
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063544
; PRIOR FILING DATE: 1997-10-28
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 408
; LENGTH: 448
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-199-672-408

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Query Match          99.8%; Score 2401; DB 12; Length 448;
Best Local Similarity 99.8%; Pred. No. 9.9e-183;
Matches 422; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy      1 QCTNGFDLDRQSGQCLDIDECRTIPEACRGDMMCVNQNGGYLCIPRTNPVYRGPYSNPYS 60
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Db      26 QCTNGFDLDRQSGQCLDIDECRTIPEACRGDMMCVNQNGGYLCIPRTNPVYRGPYSNPYS 85
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Qy      61 TPYSGPYPAAPPLSAPNYPTISRPLICRFGYQMDESNQCVDVDECATDSHQCNPTQICI 120
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Db	146		NTGGYTCSC	TDGYWLL	EGQCLDI	DECRYGYC	QQLCANV	PGSYSCT	CNPGFTL	NEDGRSC	205		
Qy	181		QDVNECAT	ENPCVQT	CVNTYGS	FI	CRCDPGY	ELEEDGV	HCS	DMDECSF	SEFLCQ	HECVNQ	240
Db	206		QDVNECAT	ENPCVQT	CVNTYGS	LI	CRCDPGY	ELEEDGV	HCS	DMDECSF	SEFLCQ	HECVNQ	265
Qy	241		PGTYFCSC	PPGYILL	DDNRSCQ	DINECEH	RNHTCN	LQOTCYN	LQGGFK	CIDPIR	CEEPYL	300	
Db	266		PGTYFCSC	PPGYILL	DDNRSCQ	DINECEH	RNHTCN	LQOTCYN	LQGGFK	CIDPIR	CEEPYL	325	
Qy	301		RISDNRCM	CPAENPG	CRDQPFT	ILYRDM	DVVSGR	SVPADIF	QMQATT	RYPGAY	YIFQIKS	360	
Db	326		RISDNRCM	CPAENPG	CRDQPFT	ILYRDM	DVVSGR	SVPADIF	QMQATT	RYPGAY	YIFQIKS	385	
Qy	361		GNEGREFY	MRQTGP	ISATLV	MTRPIK	GPRIQL	DLEMIT	VTNTVIN	FRGSSV	IRLRIY	VVSQ	420
Db	386		GNEGREFY	MRQTGP	ISATLV	MTRPIK	GPRIQL	DLEMIT	VTNTVIN	FRGSSV	IRLRIY	VVSQ	445
Qy	421		YPF	423									
Db	446		YPF	448									

RESULT 6

US-10-187-749-408

; Sequence 408, Application US/10187749

; Publication No. US20030153036A1

; GENERAL INFORMATION:

; APPLICANT: Baker, Kevin P.

; APPLICANT: Chen, Jian

; APPLICANT: Desnoyers, Luc

; APPLICANT: Goddard, Audrey

; APPLICANT: Godowski, Paul J.

; APPLICANT: Gurney, Austin L.

; APPLICANT: Pan, James

; APPLICANT: Smith, Victoria

; APPLICANT: Watanabe, Colin K.

; APPLICANT: Wood, William I.

; APPLICANT: Zhang, Zemin

; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC

; TITLE OF INVENTION: ACIDS ENCODING THE SAME

; FILE REFERENCE: P3430R1C1

; CURRENT APPLICATION NUMBER: US/10/187,749

; CURRENT FILING DATE: 2002-07-01

; PRIOR APPLICATION NUMBER: US/10/052,586

; PRIOR FILING DATE: 2002-01-15

; PRIOR APPLICATION NUMBER: 60/059263

; PRIOR FILING DATE: 1997-09-18

; PRIOR APPLICATION NUMBER: 60/059266

; PRIOR FILING DATE: 1997-09-18

; PRIOR APPLICATION NUMBER: 60/062250

; PRIOR FILING DATE: 1997-10-17

; PRIOR APPLICATION NUMBER: 60/063120

; PRIOR FILING DATE: 1997-10-24

; PRIOR APPLICATION NUMBER: 60/063121

; PRIOR FILING DATE: 1997-10-24

```

; PRIOR APPLICATION NUMBER: 60/063486
; PRIOR FILING DATE: 1997-10-21
; PRIOR APPLICATION NUMBER: 60/063540
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063541
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063544
; PRIOR FILING DATE: 1997-10-28
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 408
;   LENGTH: 448
;   TYPE: PRT
;   ORGANISM: Homo Sapien
US-10-187-749-408

```

```

Query Match          99.8%; Score 2401; DB 12; Length 448;
Best Local Similarity 99.8%; Pred. No. 9.9e-183;
Matches 422; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

```

Qy      1 QCTNGFDLDRQSGQCLDIDECRTIPEACRGDMMCVNQNGGYLCIPRTNPVYRGYPYNSNPYS 60
      |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      26 QCTNGFDLDRQSGQCLDIDECRTIPEACRGDMMCVNQNGGYLCIPRTNPVYRGYPYNSNPYS 85

Qy      61 TPYSGPYPAAPPLSAPNYPTISRPLICRFGYQMDASNQCVDVDECATDSHQCNPTQICI 120
      |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      86 TPYSGPYPAAPPLSAPNYPTISRPLICRFGYQMDASNQCVDVDECATDSHQCNPTQICI 145

Qy     121 NTEGGYTCSCTDGYWLLEGQCLDIDECRYGYCQQLCANVPGSYSCTCNPGFTLNEDGRSC 180
      |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     146 NTEGGYTCSCTDGYWLLEGQCLDIDECRYGYCQQLCANVPGSYSCTCNPGFTLNEDGRSC 205

Qy     181 QDVNECATENPCVQTCVNTYGSFICRCDPGYELEEDGVHCSDMDECSFSEFLCQHECVNQ 240
      |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     206 QDVNECATENPCVQTCVNTYGSFICRCDPGYELEEDGVHCSDMDECSFSEFLCQHECVNQ 265

Qy     241 PGTYFCSCPPGYILLDDNRSCQDINECEHRNHTCNLQQTCYNLQGGFKCIDPIRCEEPYL 300
      |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     266 PGTYFCSCPPGYILLDDNRSCQDINECEHRNHTCNLQQTCYNLQGGFKCIDPIRCEEPYL 325

Qy     301 RISDNRCMCPAENPGCRDQPFTILYRDMDVVSGRSVPADIFQMQUATTRYPGAYYIFQIKS 360
      |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     326 RISDNRCMCPAENPGCRDQPFTILYRDMDVVSGRSVPADIFQMQUATTRYPGAYYIFQIKS 385

Qy     361 GNEGREFYMRQTGPISATLVMTRPIKGPREIQLDLEMITVNTVINFRGSSVIRLRIYVSQ 420
      |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     386 GNEGREFYMRQTGPISATLVMTRPIKGPREIQLDLEMITVNTVINFRGSSVIRLRIYVSQ 445

Qy     421 YPF 423
      |||
Db     446 YPF 448

```

```

RESULT 7
US-10-194-457-408
; Sequence 408, Application US/10194457
; Publication No. US20030153037A1

```



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; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3430R1C296
; CURRENT APPLICATION NUMBER: US/10/194,457
; CURRENT FILING DATE: 2002-07-11
; PRIOR APPLICATION NUMBER: 10/052586
; PRIOR FILING DATE: 2002-01-15
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059266
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063120
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063121
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063486
; PRIOR FILING DATE: 1997-10-21
; PRIOR APPLICATION NUMBER: 60/063540
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063541
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063544
; PRIOR FILING DATE: 1997-10-28
; Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 408
; LENGTH: 448
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-194-457-408

```

```

Query Match          99.8%; Score 2401; DB 12; Length 448;
Best Local Similarity 99.8%; Pred. No. 9.9e-183;
Matches 422; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

```

QY      1 QCTNGFDLDRQSGQCLDIDECRTIPEACRGDMMCVNQNGGYLCIPRTNPVYRGPYSNPYS 60
      |||||||||||||||||||||||||||||||||||||||||||||||||||
Db      26 QCTNGFDLDRQSGQCLDIDECRTIPEACRGDMMCVNQNGGYLCIPRTNPVYRGPYSNPYS 85

QY      61 TPYSGPYPAAPPLSAPNYPTISRPLICRFGYQMDESNQCVDVDECATDSHCNPTQICI 120
      |||||||||||||||||||||||||||||||||||||||||||||||||||
Db      86 TPYSGPYPAAPPLSAPNYPTISRPLICRFGYQMDESNQCVDVDECATDSHCNPTQICI 145

```

Qy 121 NTEGGYTCSTDGYWLLEGQCLDIDECRYGYCQQLCANVPGSYSCTCNPGFTLNEDGRSC 180
 |||
 Db 146 NTEGGYTCSTDGYWLLEGQCLDIDECRYGYCQQLCANVPGSYSCTCNPGFTLNEDGRSC 205
 Qy 181 QDVNECATENPCVQTCVNTYGSFICRCDPGYELEEDGVHCSDMDECSFSEFLCQHECVNQ 240
 |||
 Db 206 QDVNECATENPCVQTCVNTYGSFICRCDPGYELEEDGVHCSDMDECSFSEFLCQHECVNQ 265
 Qy 241 PGTYFCSCPPGYILLDDNRSCQDINECEHRNHTCNLQOTCYNLQGGFKCIDPIRCEEPYL 300
 |||
 Db 266 PGTYFCSCPPGYILLDDNRSCQDINECEHRNHTCNLQOTCYNLQGGFKCIDPIRCEEPYL 325
 Qy 301 RISDNRCMCPAENPGCRDQPFTILYRDMDVVSGRSVPADIFQMQATTRYPGAYYIFQIKS 360
 |||
 Db 326 RISDNRCMCPAENPGCRDQPFTILYRDMDVVSGRSVPADIFQMQATTRYPGAYYIFQIKS 385
 Qy 361 GNEGREFYMRQTGPISATLVMTRPIKGPRIQLDLEMITVNTVINFRGSSVIRLRIYVSQ 420
 |||
 Db 386 GNEGREFYMRQTGPISATLVMTRPIKGPRIQLDLEMITVNTVINFRGSSVIRLRIYVSQ 445
 Qy 421 YPF 423
 |||
 Db 446 YPF 448

RESULT 8

US-10-184-642-408

; Sequence 408, Application US/10184642

; Publication No. US20030157635A1

; GENERAL INFORMATION:

; APPLICANT: Baker, Kevin P.

; APPLICANT: Chen, Jian

; APPLICANT: Desnoyers, Luc

; APPLICANT: Goddard, Audrey

; APPLICANT: Godowski, Paul J.

; APPLICANT: Gurney, Austin L.

; APPLICANT: Pan, James

; APPLICANT: Smith, Victoria

; APPLICANT: Watanabe, Colin K.

; APPLICANT: Wood, William I.

; APPLICANT: Zhang, Zemin

; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC

; TITLE OF INVENTION: ACIDS ENCODING THE SAME

; FILE REFERENCE: P3430R1C194

; CURRENT APPLICATION NUMBER: US/10/184,642

; CURRENT FILING DATE: 2002-06-27

; Prior Application removed - See File Wrapper or Palm

; NUMBER OF SEQ ID NOS: 612

; SEQ ID NO 408

; LENGTH: 448

; TYPE: PRT

; ORGANISM: Homo Sapien

US-10-184-642-408

Query Match 99.8%; Score 2401; DB 12; Length 448;
 Best Local Similarity 99.8%; Pred. No. 9.9e-183;
 Matches 422; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy	1	QCTNGFDLDRQSGQCLDIDECRTIPEACRGDMMCVNQNGGYLCIPRTNPVYRGPYSNPYS	60
Db	26	QCTNGFDLDRQSGQCLDIDECRTIPEACRGDMMCVNQNGGYLCIPRTNPVYRGPYSNPYS	85
Qy	61	TPYSGPYAAAPPLSAPNYPTISRPLICRFGYQMDESNQCVDVDECATDSHQCNPQTQICI	120
Db	86	TPYSGPYAAAPPLSAPNYPTISRPLICRFGYQMDESNQCVDVDECATDSHQCNPQTQICI	145
Qy	121	NTEGGYTCSTDGYWLLEGQCLDIDECRYGYCQQLCANVPGSYSCTCNPGF TLNEDGRSC	180
Db	146	NTEGGYTCSTDGYWLLEGQCLDIDECRYGYCQQLCANVPGSYSCTCNPGF TLNEDGRSC	205
Qy	181	QDVNECATENPCVQTCVNTYGSFICRCDPGYELEEDGVHCSDMDECSFSEFLCQHECVNQ	240
Db	206	QDVNECATENPCVQTCVNTYGSFICRCDPGYELEEDGVHCSDMDECSFSEFLCQHECVNQ	265
Qy	241	PGTYFCSCPPGYILLDDNRSCQDINECEHRNHTCNLQQTCYNLQGGFKCIDPIRCEEPYL	300
Db	266	PGTYFCSCPPGYILLDDNRSCQDINECEHRNHTCNLQQTCYNLQGGFKCIDPIRCEEPYL	325
Qy	301	RISDNRCMCPAENPGCRDQPF TILYRDMDVVSGRSVPADIFQM QATTRYPGAYYIFQIKS	360
Db	326	RISDNRCMCPAENPGCRDQPF TILYRDMDVVSGRSVPADIFQM QATTRYPGAYYIFQIKS	385
Qy	361	GNEGREFYMRQTGPISATLVMTRPIKGP REIQLDLEMITVNTVINFRGSSVIRLRIYVSQ	420
Db	386	GNEGREFYMRQTGPISATLVMTRPIKGP REIQLDLEMITVNTVINFRGSSVIRLRIYVSQ	445
Qy	421	YPF 423	
Db	446	YPF 448	

RESULT 9

US-10-196-747-408

; Sequence 408, Application US/10196747

; Publication No. US20030162250A1

; GENERAL INFORMATION:

; APPLICANT: Baker, Kevin P.

; APPLICANT: Chen, Jian

; APPLICANT: Desnoyers, Luc

; APPLICANT: Goddard, Audrey

; APPLICANT: Godowski, Paul J.

; APPLICANT: Gurney, Austin L.

; APPLICANT: Pan, James

; APPLICANT: Smith, Victoria

; APPLICANT: Watanabe, Colin K.

; APPLICANT: Wood, William I.

; APPLICANT: Zhang, Zemin

; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC

; TITLE OF INVENTION: ACIDS ENCODING THE SAME

; FILE REFERENCE: P3430R1C346

; CURRENT APPLICATION NUMBER: US/10/196,747

; CURRENT FILING DATE: 2002-07-16

; Prior Application removed - See File Wrapper or Palm

; NUMBER OF SEQ ID NOS: 612

; SEQ ID NO 408
; LENGTH: 448
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-196-747-408

Query Match 99.8%; Score 2401; DB 12; Length 448;
Best Local Similarity 99.8%; Pred. No. 9.9e-183;
Matches 422; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```
Qy      1 QCTNGFDLDRQSGQCLDIDECRTIPEACRGDMMCVNQNGGYLCIPRTNPVYRGPYSNPYS 60
      |||
Db      26 QCTNGFDLDRQSGQCLDIDECRTIPEACRGDMMCVNQNGGYLCIPRTNPVYRGPYSNPYS 85

Qy      61 TPYSGPYPAAPPLSAPNYPTISRPLICRFGYQMDESNQCVDVDECATDSHCNPTQICI 120
      |||
Db      86 TPYSGPYPAAPPLSAPNYPTISRPLICRFGYQMDESNQCVDVDECATDSHCNPTQICI 145

Qy     121 NTEGGYTCSCTDGYWLLEGQCLDIDECRYGYCQQLCANVPGSYSCTCNPGFTLNEDGRSC 180
      |||
Db     146 NTEGGYTCSCTDGYWLLEGQCLDIDECRYGYCQQLCANVPGSYSCTCNPGFTLNEDGRSC 205

Qy     181 QDVNECATENPCVQTCVNTYGSFICRCDPGYELEEDGVHCSDMDECSFSEFLCQHECVNQ 240
      |||
Db     206 QDVNECATENPCVQTCVNTYGSFICRCDPGYELEEDGVHCSDMDECSFSEFLCQHECVNQ 265

Qy     241 PGTYFCSCPPGYILLDDNRSCQDINECEHRNHTCNLQQTTCYNLQGGFKCIDPIRCEEPYL 300
      |||
Db     266 PGTYFCSCPPGYILLDDNRSCQDINECEHRNHTCNLQQTTCYNLQGGFKCIDPIRCEEPYL 325

Qy     301 RISDNRCMCPAENPGCRDQPFTILYRDMDVVSGRSVPADIFQMQATTRYPGAYYIFQIKS 360
      |||
Db     326 RISDNRCMCPAENPGCRDQPFTILYRDMDVVSGRSVPADIFQMQATTRYPGAYYIFQIKS 385

Qy     361 GNEGREFYMRQTGPISATLVMTRPIKGPREIQLDLEMITVNTVINFRGSSVIRLRIYVSQ 420
      |||
Db     386 GNEGREFYMRQTGPISATLVMTRPIKGPREIQLDLEMITVNTVINFRGSSVIRLRIYVSQ 445

Qy     421 YPF 423
      |||
Db     446 YPF 448
```

RESULT 10

US-10-173-689-408

; Sequence 408, Application US/10173689
; Publication No. US20030166104A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.

```

; APPLICANT: Wood,William I.
; APPLICANT: Zhang,Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3430R1C10
; CURRENT APPLICATION NUMBER: US/10/173,689
; CURRENT FILING DATE: 2002-06-17
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 408
; LENGTH: 448
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-173-689-408

```

```

Query Match          99.8%; Score 2401; DB 12; Length 448;
Best Local Similarity 99.8%; Pred. No. 9.9e-183;
Matches 422; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

```

Qy      1 QCTNGFDLDRQSGQCLDIDECRTIPEACRGDMMCVNQNGGYLCIPRTNPVYRGYPYNSNPYS 60
      |||
Db      26 QCTNGFDLDRQSGQCLDIDECRTIPEACRGDMMCVNQNGGYLCIPRTNPVYRGYPYNSNPYS 85

Qy      61 TPYSGPYPAAPPLSAPNYPTISRPLICRFGYQMDENQCVDVDECATDSHQCNPTQICI 120
      |||
Db      86 TPYSGPYPAAPPLSAPNYPTISRPLICRFGYQMDENQCVDVDECATDSHQCNPTQICI 145

Qy     121 NTEGGYTCSTDGWLLLEGQCLDIDECRYGYCQQLCANVPGSYSCTCNPGFTLNEDGRSC 180
      |||
Db     146 NTEGGYTCSTDGWLLLEGQCLDIDECRYGYCQQLCANVPGSYSCTCNPGFTLNEDGRSC 205

Qy     181 QDVNECATENPCVQTCVNTYGSFICRCDPGYELEEDGVHCSDMDECSFSEFLCQHECVNQ 240
      |||
Db     206 QDVNECATENPCVQTCVNTYGSFICRCDPGYELEEDGVHCSDMDECSFSEFLCQHECVNQ 265

Qy     241 PGTYFCS CPPGYILLDDNRSCQDINECEHRNHTCNLQQTTCYNLQGGFKCIDPIRCEEPYL 300
      |||
Db     266 PGTYFCS CPPGYILLDDNRSCQDINECEHRNHTCNLQQTTCYNLQGGFKCIDPIRCEEPYL 325

Qy     301 RISDNRCMCPAENPGCRDQPFTILYRDMDVVSGRSVPADIFQM QATTRYPGAYYIFQIKS 360
      |||
Db     326 RISDNRCMCPAENPGCRDQPFTILYRDMDVVSGRSVPADIFQM QATTRYPGAYYIFQIKS 385

Qy     361 GNEGREFYMRQTGPISATLVMTRPIKGPRIQLDLEMITVNTVINFRGSSVIRLRIYVSQ 420
      |||
Db     386 GNEGREFYMRQTGPISATLVMTRPIKGPRIQLDLEMITVNTVINFRGSSVIRLRIYVSQ 445

Qy     421 YPF 423
      |||
Db     446 YPF 448

```

RESULT 11

```

US-10-173-690-408
; Sequence 408, Application US/10173690
; Publication No. US20030166105A1
; GENERAL INFORMATION:

```

```
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3430R1C9
; CURRENT APPLICATION NUMBER: US/10/173,690
; CURRENT FILING DATE: 2002-06-17
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 408
; LENGTH: 448
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-173-690-408
```

```
Query Match          99.8%; Score 2401; DB 12; Length 448;
Best Local Similarity 99.8%; Pred. No. 9.9e-183;
Matches 422; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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```
Qy      1 QCTNGFDLDRQSGQCLDIDECRTIPEACRGDMMCVNQNGGYLCIPRTNPVYRGPYSNPYS 60
      |||
Db      26 QCTNGFDLDRQSGQCLDIDECRTIPEACRGDMMCVNQNGGYLCIPRTNPVYRGPYSNPYS 85

Qy      61 TPYSGPYPAAPPLSAPNYPTISRPLICRFGYQMDESNQCDVDECATDSHQCNPQTQICI 120
      |||
Db      86 TPYSGPYPAAPPLSAPNYPTISRPLICRFGYQMDESNQCDVDECATDSHQCNPQTQICI 145

Qy     121 NTEGGYTCSCTDGYWLLEGQCLDIDECRYGYCQQLCANVPGSYSCTCNPGFTLNEDGRSC 180
      |||
Db     146 NTEGGYTCSCTDGYWLLEGQCLDIDECRYGYCQQLCANVPGSYSCTCNPGFTLNEDGRSC 205

Qy     181 QDVNECATENPCVQTCVNTYGSFICRCDPGYELEEDGVHCSDMDECSFSEFLCQHECVNQ 240
      |||
Db     206 QDVNECATENPCVQTCVNTYGSFICRCDPGYELEEDGVHCSDMDECSFSEFLCQHECVNQ 265

Qy     241 PGTYFCSCPPGYILLDDNRSCQDINECEHRNHTCNLQQTTCYNLQGGFKCIDPIRCEEPYL 300
      |||
Db     266 PGTYFCSCPPGYILLDDNRSCQDINECEHRNHTCNLQQTTCYNLQGGFKCIDPIRCEEPYL 325

Qy     301 RISDNRCMCPAENPGCRDQPFTILYRDMDVVSGRSVPADIFQMQATTRYPGAYYIFQIKS 360
      |||
Db     326 RISDNRCMCPAENPGCRDQPFTILYRDMDVVSGRSVPADIFQMQATTRYPGAYYIFQIKS 385

Qy     361 GNEGREFYMRQTGPISATLVMTRPIKGPREIQLDLEMITVNTVINFRGSSVIRLRIYVSQ 420
      |||
Db     386 GNEGREFYMRQTGPISATLVMTRPIKGPREIQLDLEMITVNTVINFRGSSVIRLRIYVSQ 445

Qy     421 YPF 423
```

Db |||
446 YPF 448

RESULT 12
US-10-173-691-408
; Sequence 408, Application US/10173691
; Publication No. US20030166106A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3430R1C13
; CURRENT APPLICATION NUMBER: US/10/173,691
; CURRENT FILING DATE: 2002-06-17
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 408
; LENGTH: 448
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-173-691-408

Query Match 99.8%; Score 2401; DB 12; Length 448;
Best Local Similarity 99.8%; Pred. No. 9.9e-183;
Matches 422; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy	1	QCTNGFDLDRQSGQCLDIDECRTIPEACRGDMMCVNQNGGYLCIPRTNPVYRGPYSNPYS	60
Db	26	QCTNGFDLDRQSGQCLDIDECRTIPEACRGDMMCVNQNGGYLCIPRTNPVYRGPYSNPYS	85
Qy	61	TPYSGPYPAAPPLSAPNYPTISRPLICRFGYQMDESNQCVDVDECATDSHQCNPQTQICI	120
Db	86	TPYSGPYPAAPPLSAPNYPTISRPLICRFGYQMDESNQCVDVDECATDSHQCNPQTQICI	145
Qy	121	NTEGGYTCSCTDGYWLLEGQCLDIDECRYGYCQQLCANVPGSYSCTCNPGFTLNEDGRSC	180
Db	146	NTEGGYTCSCTDGYWLLEGQCLDIDECRYGYCQQLCANVPGSYSCTCNPGFTLNEDGRSC	205
Qy	181	QDVNECATENPCVQTCVNTYGSFICRCDPGYELEEDGVHCSDMDECSFSEFLCQHECVNQ	240
Db	206	QDVNECATENPCVQTCVNTYGSFICRCDPGYELEEDGVHCSDMDECSFSEFLCQHECVNQ	265
Qy	241	PGTYFCSCPPGYILLDDNRSCQDINECEHRNHTCNLQQTCYNLQGGFKCIDPIRCEEPYL	300
Db	266	PGTYFCSCPPGYILLDDNRSCQDINECEHRNHTCNLQQTCYNLQGGFKCIDPIRCEEPYL	325

Qy	301	RISDNRCMCPAENPGCRDQPF	TILYRDMDVVSGRSVPADIFQM	QATTRYPGAYYIFQIKS	360	
Db	326	RISDNRCMCPAENPGCRDQPF	TILYRDMDVVSGRSVPADIFQM	QATTRYPGAYYIFQIKS	385	
Qy	361	GNEGREFYMRQTGPISATLVM	TRPIKGP	PREIQLDLEMITVNTVINFRG	SSVIRLRIYVSQ	420
Db	386	GNEGREFYMRQTGPISATLVM	TRPIKGP	PREIQLDLEMITVNTVINFRG	SSVIRLRIYVSQ	445
Qy	421	YPF	423			
Db	446	YPF	448			

Query Match 99.8%; Score 2401; DB 12; Length 448;
Best Local Similarity 99.8%; Pred. No. 9.9e-183;
Matches 422; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy	181	QDVNECATENPCVQTCVNTYGSFICRCDPGYELEEDGVHCSDMDECSFSEFLCQHECVNQ	240
Db	206	QDVNECATENPCVQTCVNTYGSLICRCDPGYELEEDGVHCSDMDECSFSEFLCQHECVNQ	265
Qy	241	PGTYFCSCPPGYILLDDNRSCQDINECEHRNHTCNLQQTCYNLQGGFKCIDPIRCEEPYL	300
Db	266	PGTYFCSCPPGYILLDDNRSCQDINECEHRNHTCNLQQTCYNLQGGFKCIDPIRCEEPYL	325
Qy	301	RISDNRCMCPAENPGCRDQPFTILYRDMDVVSGRSVPADIFQMQATTRYPGAYYIFQIKS	360
Db	326	RISDNRCMCPAENPGCRDQPFTILYRDMDVVSGRSVPADIFQMQATTRYPGAYYIFQIKS	385
Qy	361	GNEGREFYMRQTGPISATLVMTRPIKGPRIQLDLEMITVNTVINFRGSSVIRLRIYVSQ	420
Db	386	GNEGREFYMRQTGPISATLVMTRPIKGPRIQLDLEMITVNTVINFRGSSVIRLRIYVSQ	445
Qy	421	YPF	423
Db	446	YPF	448

RESULT 14

US-10-173-694-408

; Sequence 408, Application US/10173694

; Publication No. US20030166107A1

; GENERAL INFORMATION:

; APPLICANT: Baker, Kevin P.

; APPLICANT: Chen, Jian

; APPLICANT: Desnoyers, Luc

; APPLICANT: Goddard, Audrey

; APPLICANT: Godowski, Paul J.

; APPLICANT: Gurney, Austin L.

; APPLICANT: Pan, James

; APPLICANT: Smith, Victoria

; APPLICANT: Watanabe, Colin K.

; APPLICANT: Wood, William I.

; APPLICANT: Zhang, Zemin

; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC

; TITLE OF INVENTION: ACIDS ENCODING THE SAME

; FILE REFERENCE: P3430R1C19

; CURRENT APPLICATION NUMBER: US/10/173,694

; CURRENT FILING DATE: 2002-06-17

; Prior Application removed - See File Wrapper or Palm

; NUMBER OF SEQ ID NOS: 612

; SEQ ID NO 408

; LENGTH: 448

; TYPE: PRT

; ORGANISM: Homo Sapien

US-10-173-694-408

Query Match 99.8%; Score 2401; DB 12; Length 448;

Best Local Similarity 99.8%; Pred. No. 9.9e-183;

Matches 422; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy	1	QCTNGFDLDRQSGQCLDIDECRTIPEACRGDMMCVQNQGGYLCIPRTNPVYRGPNPYS	60

Db 26 QCTNGFDLDRQSGQCLDIDECRTIPEACRGDMMCVNQNGGYLCIPRTNPVYRGPYSNPYS 85
 Qy 61 TPYSGPYPAAPPLSAPNYPTISRPLICRFGYQMDESNQCVDVDECATDSHQCNPTQICI 120
 |||||
 Db 86 TPYSGPYPAAPPLSAPNYPTISRPLICRFGYQMDESNQCVDVDECATDSHQCNPTQICI 145
 Qy 121 NTEGGYTCSCTDGYWLLEGQCLDIDECRYGYCQQLCANVPGSYSCTCNPGFTLNEDGRSC 180
 |||||
 Db 146 NTEGGYTCSCTDGYWLLEGQCLDIDECRYGYCQQLCANVPGSYSCTCNPGFTLNEDGRSC 205
 Qy 181 QDVNECATENPCVQTCVNTYGSFICRCDPGYELEEDGVHCSDMDECSFSEFLCQHECVNQ 240
 |||||
 Db 206 QDVNECATENPCVQTCVNTYGSFICRCDPGYELEEDGVHCSDMDECSFSEFLCQHECVNQ 265
 Qy 241 PGTYFCSCPPGYILLDDNRSCQDINECEHRNHTCNLQQTTCYNLQGGFKCIDPIRCEEPYL 300
 |||||
 Db 266 PGTYFCSCPPGYILLDDNRSCQDINECEHRNHTCNLQQTTCYNLQGGFKCIDPIRCEEPYL 325
 Qy 301 RISDNRCMCPAENPGCRDQPFTILYRDMDVVSGRSVPADIFQMQATTRYPGAYYIFQIKS 360
 |||||
 Db 326 RISDNRCMCPAENPGCRDQPFTILYRDMDVVSGRSVPADIFQMQATTRYPGAYYIFQIKS 385
 Qy 361 GNEGREFYMRQTGPISATLMTRPIKGPRIQLDLEMITVNTVINFRGSSVIRLRIYVSQ 420
 |||||
 Db 386 GNEGREFYMRQTGPISATLMTRPIKGPRIQLDLEMITVNTVINFRGSSVIRLRIYVSQ 445
 Qy 421 YPF 423
 |||
 Db 446 YPF 448

RESULT 15

US-10-173-698-408

; Sequence 408, Application US/10173698

; Publication No. US20030166108A1

; GENERAL INFORMATION:

; APPLICANT: Baker, Kevin P.

; APPLICANT: Chen, Jian

; APPLICANT: Desnoyers, Luc

; APPLICANT: Goddard, Audrey

; APPLICANT: Godowski, Paul J.

; APPLICANT: Gurney, Austin L.

; APPLICANT: Pan, James

; APPLICANT: Smith, Victoria

; APPLICANT: Watanabe, Colin K.

; APPLICANT: Wood, William I.

; APPLICANT: Zhang, Zemin

; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC

; TITLE OF INVENTION: ACIDS ENCODING THE SAME

; FILE REFERENCE: P3430R1C12

; CURRENT APPLICATION NUMBER: US/10/173,698

; CURRENT FILING DATE: 2002-06-17

; Prior Application removed - See File Wrapper or Palm

; NUMBER OF SEQ ID NOS: 612

; SEQ ID NO 408

; LENGTH: 448

; TYPE: PRT

; ORGANISM: Homo Sapien
US-10-173-698-408

Query Match 99.8%; Score 2401; DB 12; Length 448;
Best Local Similarity 99.8%; Pred. No. 9.9e-183;
Matches 422; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy      1 QCTNGFDLDRQSGQCLDIDECRTIPEACRGDMMCVNQNGGYLCIPRTNPVYRGPYSNPYS 60
          |||
Db      26 QCTNGFDLDRQSGQCLDIDECRTIPEACRGDMMCVNQNGGYLCIPRTNPVYRGPYSNPYS 85

Qy     61 TPYSGPYPAAPPLSAPNYPTISRPLICRFGYQMDESNQCDVDECATDSHQCNPQTQICI 120
          |||
Db     86 TPYSGPYPAAPPLSAPNYPTISRPLICRFGYQMDESNQCDVDECATDSHQCNPQTQICI 145

Qy    121 NTEGGYTCSTDGWLLLEGQCLDIDECRYGYCQQLCANVPGSYSCTCNPGFTLNEDGRSC 180
          |||
Db    146 NTEGGYTCSTDGWLLLEGQCLDIDECRYGYCQQLCANVPGSYSCTCNPGFTLNEDGRSC 205

Qy    181 QDVNECATENPCVQTCVNTYGSFICRCDPGYELEEDGVHCSDMDECSFSEFLCQHECVNQ 240
          |||
Db    206 QDVNECATENPCVQTCVNTYGSFICRCDPGYELEEDGVHCSDMDECSFSEFLCQHECVNQ 265

Qy    241 PGTYFCSCPPGYILLDDNRSCQDINECEHRNHTCNLQOTCYNLQGGFKCIDPIRCEEPYL 300
          |||
Db    266 PGTYFCSCPPGYILLDDNRSCQDINECEHRNHTCNLQOTCYNLQGGFKCIDPIRCEEPYL 325

Qy    301 RISDNRCMCPAENPGCRDQPFTILYRMDVVSGRSVPADIFQMQATTRYPGAYYIFQIKS 360
          |||
Db    326 RISDNRCMCPAENPGCRDQPFTILYRMDVVSGRSVPADIFQMQATTRYPGAYYIFQIKS 385

Qy    361 GNEGREFYMRQTGPISATLVMTRPIKGPREIQLDLEMITVNTVINFRGSSVIRLRIYVSQ 420
          |||
Db    386 GNEGREFYMRQTGPISATLVMTRPIKGPREIQLDLEMITVNTVINFRGSSVIRLRIYVSQ 445

Qy    421 YPF 423
          |||
Db    446 YPF 448
```

Search completed: January 9, 2004, 12:43:59
Job time : 29.1676 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 9, 2004, 12:29:16 ; Search time 16.0264 Seconds
(without alignments)
2538.270 Million cell updates/sec

Title: US-09-674-379A-14
Perfect score: 2407
Sequence: 1 QCTNGFDLDRQSGQCLDIDE.....INFRGSSVIRLRIYVSQYPF 423

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_76:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query		DB	ID	Description
		Match	Length			
1	1108.5	46.1	493	2	JC5621	epidermal growth f
2	963.5	40.0	387	2	I38449	extracellular prot
3	744.5	30.9	685	2	S78040	fibulin, splice fo
4	735.5	30.6	683	2	C36346	fibulin 1 precurs
5	729.5	30.3	1221	2	A49457	fibulin-2 precurs
6	702	29.2	705	2	S34968	fibulin, splice fo
7	701.5	29.1	1184	2	A55184	fibulin-2 precurs
8	617.5	25.7	601	2	B36346	fibulin 1 precurs
9	603	25.1	689	2	T42760	fibulin, splice fo
10	596	24.8	712	2	T42990	fibulin 1, splice
11	592.5	24.6	589	2	T43210	fibulin-1D precurs
12	574	23.8	798	2	T22793	hypothetical prote
13	539	22.4	1394	2	A35626	transforming growt

14	523.5	21.7	3002	2	A47221	fibrillin 1 precur
15	522.5	21.7	2871	2	A55567	fibrillin I - bovi
16	518	21.5	1712	2	A38261	masking protein pr
17	509.5	21.2	2871	2	A55624	fibrillin-1 precur
18	509.5	21.2	2907	2	A57278	fibrillin-2 precur
19	508.5	21.1	2918	2	A54105	fibrillin-2 precur
20	469.5	19.5	1820	2	A55494	latent transformin
21	455	18.9	741	2	T46488	hypothetical prote
22	448.5	18.6	1620	2	T27283	hypothetical prote
23	438	18.2	1251	2	A57293	latent transformin
24	436	18.1	1574	2	T13954	MEGF6 protein - ra
25	392	16.3	886	2	A57172	probable hormone r
26	384.5	16.0	3507	2	T34513	hypothetical prote
27	368.5	15.3	1106	2	T18739	hypothetical prote
28	367	15.2	2471	2	A49128	cell-fate determin
29	364	15.1	810	2	T10756	Nel-homolog protei
30	361	15.0	1081	2	T31329	receptor tyrosine
31	359	14.9	1203	2	A49175	Motch B protein -
32	356	14.8	2555	2	A40043	notch protein homo
33	353.5	14.7	1964	2	T09059	notch4 - mouse
34	351.5	14.6	2437	2	S42612	transmembrane prot
35	348.5	14.5	2703	1	A24420	notch protein - fr
36	340.5	14.1	673	2	A48089	growth arrest-spec
37	340	14.1	2524	2	A35844	Xotch protein - Af
38	335.5	13.9	2531	2	S18188	notch protein homo
39	335	13.9	674	2	I55476	growth potentiatin
40	334	13.9	511	2	T17298	hypothetical prote
41	334	13.9	2531	2	T31070	notch homolog - se
42	333	13.8	1064	2	A40136	fibropellin Ia - s
43	333	13.8	2321	2	S78549	notch3 protein - h
44	325.5	13.5	2531	2	A46019	notch-1 protein -
45	324.5	13.5	2318	2	S45306	notch 3 protein -

ALIGNMENTS

RESULT 1

JC5621

epidermal growth factor-like protein, T16 precursor - rat

C;Species: Rattus norvegicus (Norway rat)

C;Date: 09-Oct-1997 #sequence_revision 07-Nov-1997 #text_change 05-Nov-1999

C;Accession: JC5621

R;Ozaki, T.; Kondo, K.; Nakamura, Y.; Ichimiya, S.; Nakagawara, A.; Sakiyama, S.
Biochem. Biophys. Res. Commun. 237, 245-250, 1997

A;Title: Interaction of DA41, a DAN-binding protein, with the epidermal growth factor-like protein, S(1-5).

A;Reference number: JC5621; MUID:97415782; PMID:9268694

A;Accession: JC5621

A;Molecule type: mRNA

A;Residues: 1-493 <OZA>

A;Cross-references: DDBJ:D89730; NID:g2429082; PIDN:BAA22265.1; PID:d1023127; PID:g2429083

C;Comment: This protein plays a role in the regulation of cell growth by interacting with DAN protein through DA41 protein.

C;Keywords: glycoprotein

F;1-17/Domain: signal sequence #status predicted <SIG>

A;Cross-references: EMBL:U03877; NID:g458227; PIDN:AAA65590.1; PID:g458228
C;Genetics:
A;Gene: S1-5

Query Match 40.0%; Score 963.5; DB 2; Length 387;
Best Local Similarity 48.3%; Pred. No. 1.9e-56;
Matches 171; Conservative 55; Mismatches 123; Indels 5; Gaps 4;

```
Qy      71 APPLSAPNYPTISRPLICRFGYQMDESNQCVDVDECATDSHCNPTQICINTEGGYTCS 130
      | | | | | : | | | : | | | : | | | : | | | : | | |
Db      38 ADPQRIPSNP--SHRIQCAAGYEQSEHNVCQDIDECTAGTHNCRADQVCINLRGSFACQC 95

Qy     131 TDGYWLLEGQCLDIDECRY-GYCQQLCANVPGSYSCTCNPGFTLNEDGRSCQDVNECATE 189
      | | | | | | | | | | | | | | | | | | | | | | | | |
Db      96 PPGYQKRGEQCVDIDECTIPPYCHQRCVNTPGSFYQCSPGFQLAANNYTCVDINECDAS 155

Qy     190 NPCVQTCVNTYGSFICRCDPGYELEEDGVHCSDMDECSFSEFLCQHECVNQPGETYFCSCP 249
      | | | | | | | | | | | | | | | | | | | | | | | | |
Db     156 NQCAQQCYNILGSFICQCNQGYELSSDRLNCEDIDECRTSSYLCQYQCVNEPGKFSCMCP 215

Qy     250 PGYILLDDNRSCQDINECEHRNHTCNLQQTCYNLQGGFKCIDPIRCEEYPYLRISDNRCMC 309
      | | : : : | | | | | | | | | | | | | | | | | | | |
Db     216 QGYQVV-RSRTCQDINECETTNE-CREDEMCWNYHGGFRCYPRNPCQDPYILTPEINRCVC 273

Qy     310 PAENPGCRDQPFITILYRDMDVVSGRSVPADIFQMQATTRYPGAYYIFQIKSGNEGREFYM 369
      | | | | | : | : | : | : | | | | | | | | | | | | |
Db     274 PVSNAMELPQSIVYKYMSIRSDRSVPSDIFQIQATTIYANTINTFRIKSGNENGFEFYL 333

Qy     370 RQTGPISATLVMTRPIKGPRIQLDLEMITVNTVINFRGSSVIRLRIYVSQYPF 423
      | | | | : | | | | : : | | | | : | | | | : | | | |
Db     334 RQTSPVSAMLVLVKSLSGPREHIVDLEMLTVSSIGTFRTSSVLRLTIIVGPFSF 387
```

RESULT 3

S78040

fibulin, splice form C precursor - mouse

N;Alternate names: basement-membrane protein BM-90

C;Species: Mus musculus (house mouse)

C;Date: 24-Jul-1998 #sequence_revision 24-Jul-1998 #text_change 02-Aug-2002

C;Accession: S78040; S78560; S36440

R;Pan, T.C.; Kluge, M.; Zhang, R.Z.; Mayer, U.; Timpl, R.; Chu, M.L.

Eur. J. Biochem. 215, 733-740, 1993

A;Title: Sequence of extracellular mouse protein BM-90/fibulin and its calcium-dependent binding to other basement-membrane ligands.

A;Reference number: S34968; MUID:93358897; PMID:8354280

A;Accession: S78040

A;Molecule type: mRNA

A;Residues: 1-685 <PAN>

A;Cross-references: EMBL:X70854

R;Pan, T.C.; Kluge, M.; Zhang, R.Z.; Mayer, U.; Timpl, R.; Chu, M.L.

submitted to the EMBL Data Library, January 1993

A;Description: Sequence of extracellular mouse protein BM-90/fibulin and its calcium-dependent binding to other basement membrane ligands.

A;Reference number: S36440

A;Accession: S78560

A;Molecule type: mRNA

A;Residues: 1-39,'P',41-685 <CHU>

A;Cross-references: EMBL:X70854
 C;Genetics:
 A;Introns: 568/3
 C;Superfamily: fibulin-1; EGF homology
 C;Keywords: alternative splicing; basement membrane; calcium binding;
 extracellular matrix; glycoprotein; plasma
 F;1-29/Domain: signal sequence #status predicted <SIG>
 F;30-685/Product: fibulin, splice form C #status predicted <MAT>
 F;98,537,541/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 30.9%; Score 744.5; DB 2; Length 685;
 Best Local Similarity 36.6%; Pred. No. 8.3e-42;
 Matches 159; Conservative 63; Mismatches 151; Indels 61; Gaps 16;

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Qy      1 QCTNGFDLDRQSGQCLDIDECRTIPEACRGDMMCVNQNGGYLCIPRTNPVYRGPYSNPYS 60
      || :|| | | :||:| | :| | | | | | | | |
Db      295 QCKSGFIQD-ALGNCIDINECLSIAPCPVGQTCINTEGSYTC----- 336

Qy      61 TPYSGPYPAAPPLSAPNYPTISRPLICRFGYQM-DESNQCVDVDECATDSHCNPTQIC 119
      : || | | | : | | : ||||| | : | |
Db      337 -----QKNVPN-----CGRGYHLNEEGTRCVDVDECAPPAEPCGKGHHC 375

Qy      120 INTEGgyTCsCTDGYWL--LEGQCLDIDEC-RY--GYCQQLCANVPGSYsCTCNPGFTLN 174
      :| : | | | : : : | :| :| | | | | | | | :| :| :| | | :
Db      376 LNSPGSFRCECKAGFYFDGISRTCVDINECQRYPGRLCGHKCENTPGSFHCSCSAGFRLS 435

Qy      175 EDGRSCQDVNECATENPCVQTCVNTYGSFICRCDPGYELEEDGVHCSMDDECSF--SEF 231
      ||||:|||| | :|| | | | ||: | | ||: | : || | | :||| :
Db      436 VDGRSCEDVNEC-LNSPCSQECANVYGSYQCYCRRGYQLSDVDGVTCEDIDECALPTGGH 494

Qy      232 LCQHECVNQPGTYFCSCP-PGYILLDDNRSCQDINECEHRNHTCNLQOTCYNLQGGFKCI 290
      : | : | :| ||| | | | | : ||||:| | | | : : ||:| :| | :| :
Db      495 ICSYRCINIPGSFQCSCPSSGYRLAPNGRNCQDIDECVTGIHNCSINETCFNIQGSFRCL 554

Qy      291 DPIRCEEPYLRISDNRCM---CPAENPGCRDQPFITILYRMDVVSGRSVPADIFQMATT 347
      | | | | :| | | | | | | | | | : : | | :| :| :| :
Db      555 S-FECPENYRRSADTRCARLPC-HENQECPRPLRITYYHLSFPTNIQVPAVVFMRGPSS 612

Qy      348 RYPGAYYIFQIKSGNEGREFYMRQTGPISATLVMTRPIKGPRIQLDLEM--ITVNTVIN 405
      || | | :|| | | : | : :| :| | | :| :| :| | | :
Db      613 AVPGDSMQLAITAGNEEGFFTTRKVVSHSGVVALTKPIPEPRDLLLTVKMDLYRHGTVSS 672

Qy      406 FRGSSVIRLRIYVS 419
      | | | :| | |
Db      673 F----VAKLFIFVS 682

```

RESULT 4

C36346

fibulin 1 precursor, splice form C - human

N;Alternate names: fibulin C

N;Contains: fibulin 1 splice form A; fibulin 1 splice form C

C;Species: Homo sapiens (man)

C;Date: 19-Apr-1991 #sequence_revision 19-Apr-1991 #text_change 02-Aug-2002

C;Accession: C36346; A36346; A32826

R;Argaves, W.S.; Tran, H.; Burgess, W.H.; Dickerson, K.

J. Cell Biol. 111, 3155-3164, 1990

A;Title: Fibulin is an extracellular matrix and plasma glycoprotein with repeated domain structure.
A;Reference number: A36346; MUID:91100426; PMID:2269669
A;Accession: C36346
A;Molecule type: mRNA
A;Residues: 1-683 <ARG>
A;Cross-references: GB:X53743; NID:g31418; PIDN:CAA37772.1; PID:g31419
A;Accession: A36346
A;Molecule type: mRNA
A;Residues: 1-566 <AR2>
A;Cross-references: GB:X53741; NID:g31414; PIDN:CAA37770.1; PID:g31415
R;Argaves, W.S.; Dickerson, K.; Burgess, W.H.; Ruoslahti, E.
Cell 58, 623-629, 1989
A;Title: Fibulin, a novel protein that interacts with the fibronectin receptor beta-subunit cytoplasmic domain.
A;Reference number: A32826; MUID:89354537; PMID:2527614
A;Accession: A32826
A;Molecule type: protein
A;Residues: 30-35, 'SX', 38-40, 'SH', 43-44 <AR3>
C;Genetics:
A;Gene: GDB:FBLN1; FBLN
A;Cross-references: GDB:278285; OMIM:135820
A;Map position: 22q13.3-22q13.3
C;Superfamily: fibulin-1; EGF homology
C;Keywords: alternative splicing; glycoprotein
F;1-29/Domain: signal sequence #status predicted <SIG>
F;30-683/Product: fibulin 1 splice form C #status predicted <MAT>
F;180-214/Domain: EGF homology <EGF>
F;485-523/Domain: EGF homology <EGF1>
F;98,535,539/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 30.6%; Score 735.5; DB 2; Length 683;
Best Local Similarity 35.7%; Pred. No. 3.2e-41;
Matches 155; Conservative 66; Mismatches 152; Indels 61; Gaps 16;

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Qy      1 QCTNGFDLDRQSGQCLDIDECRTIPEACRGDMMCVNQNGGYLCIPRTNPVYRGYPYNSNPYS 60
      || :|| | | | :|||:| | :| | | | | |
Db      293 QCKSGFIQD-ALGNCIDINECLISAPCPIGHTCINTEGSYTC----- 334

Qy      61 TPYSGPYAAAPPLSAPNYPTISRPLICRFGYQM-DESNQCVDVDECATDSHCNPTQIC 119
      : || | | : | : ||||| | : | |
Db      335 -----QKNVPN-----CGRGYHLNEEGTRCVDVDECAPPAEPCGKGHRC 373

Qy      120 INTEGgyTCSCTDGYWL--LEGQCLDIDEC-RY--GYCQQLCANVPGSYSCTCNPGFTLN 174
      :|: | : | | ||: | :|:| | | | | | ||| |:|: | | |
Db      374 VNSPGSFRCECKTGYFYFDGISRMCVDVNECQRYPGRLCGHKCENTLGSYLCSCSVGFRLS 433

Qy      175 EDGRSCQDVNECATENPCVQTCVNTYGSFICRCDPGYELEE-DGVHCSMDDECSF--SEF 231
      |||||:|:||||: :|| | | | |||: | | ||:| : ||| | |:| | |
Db      434 VDGRSCEDINECSS-SPCSQECANVYGSYQYCRRGYQLSDVDGVTCEDIDECALPTGGH 492

Qy      232 LCQHECVNQPGTYFCSCP-PGYILLDDNRSCQDINECEHRNHTCNLQQTTCYNLQGGFKCI 290
      :| : | :| |||: ||| | | : | :|||:| | | | : :| :| :| | | :| :
Db      493 ICSYRCINIPGSFQCSCPSSGYRLAPNGRNCQDIDECVTGIHNCSINETCFNIQGAFRCL 552

Qy      291 DPIRCEEPYLRISDNRC-MCPA-ENPGCRDQPFITILYRDMDVVSGRSVPADIFQMQATTR 348
      | | | | : || | | | | | | : : | | :| :| :| :

```

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Db      553 -AFECPENYRRSAATRCERLPCHENRECSKLPLRITYYHLSFPTNIQAPAVVFRMGPSA 611
Qy      349 YPGAYYIFQIKSGNEGREFYMRQTGPISATLVMTRPIKGPREIQLDLEMITVNTVINFRG 408
        ||      |   ||   |   |:   |   :   :|:|:   ||::   ::||   ::   |
Db      612 VPGDSMQLAITGGNEEGFFTTRKVSPhSGVVALTKPVPEPRDL-----LLTVKMDLSRHG 666

Qy      409 ---SSVIRLRIYVS 419
        |   |   |   |   |
Db      667 TVSSFVAKLFIFVS 680

```

RESULT 5

A49457

fibulin-2 precursor - mouse

C;Species: Mus musculus (house mouse)

C;Date: 03-May-1994 #sequence_revision 03-May-1994 #text_change 08-Sep-2002

C;Accession: A49457; S74095

R;Pan, T.C.; Sasaki, T.; Zhang, R.Z.; Faessler, R.; Timpl, R.; Chu, M.L.
J. Cell Biol. 123, 1269-1277, 1993

A;Title: Structure and expression of fibulin-2, a novel extracellular matrix protein with multiple EGF-like repeats and consensus motifs for calcium binding.

A;Reference number: A49457; MUID:94064787; PMID:8245130

A;Accession: A49457

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-1221 <PAN>

A;Cross-references: GB:X75285; NID:g437046; PIDN:CAA53040.1; PID:g437047

R;Sasaki, T.; Mann, K.; Murphy, G.; Chu, M.L.; Timpl, R.

Eur. J. Biochem. 240, 427-434, 1996

A;Title: Different susceptibilities of fibulin-1 and fibulin-2 to cleavage by matrix metalloproteinases and other tissue proteases.

A;Reference number: S74094; MUID:96439073; PMID:8841408

A;Accession: S74095

A;Molecule type: protein

A;Residues: 236-238,'X',240-247;260-275;336-344,'L',346-361;405-426;566-568,'EM',569-589;653-666;784-787,'X',789-794;841-844,'X',846-850;883-892,'X',894-894;930-935,'X',937-939 <SAS>

C;Superfamily: fibulin-2; EGF homology; von Willebrand factor type C repeat homology

C;Keywords: calcium binding; duplication; extracellular matrix; glycoprotein; homotrimer

F;942-978/Domain: EGF homology <EGF>

```

Query Match          30.3%; Score 729.5; DB 2; Length 1221;
Best Local Similarity 35.3%; Pred. No. 1.3e-40;
Matches 145; Conservative 59; Mismatches 148; Indels 59; Gaps 11;

```

```

Qy      1 QCTNGFDLDRQSGQCLDIDECRTIPEACRGDMMCVNQGGYLCIPRTNPVYRGYPYNSPYS 60
        :| :|| |   | |::||| :: | ||   |:: | || |
Db      832 RCMDGF-LQDPEGNCVDINECTSLLEPCRSGFSCINTVGSYTC----- 873

Qy      61 TPYSGPYPAAPPLSAPNYPTISRPLICRFGYQM-DESNQCVDVDECATDSHQCNPTQIC 119
        ||:| ||   :| ::|||:| | | |::| |
Db      874 -----QRNPLVCGRGYHANEEGSECVDVNECETGVHRCGEGQLC 912

Qy      120 INTEGGYTCSCTDGYW--LLEGQCLDIDECRYG---YCQQLCANVPGSYSCTCNPGFTLN 174
        | | | | | | :   | :::||   || | | |||| |:: | | |

```

Db 913 YNLPGSYRCDCKPGFQRDAFGRTCIDVNECWVSPGRLCQHTCENTPGSYRCSAAGFLLA 972
 Qy 175 EDGRSCQDVNECATENPCVQTCVNTYGSFICRCDPGYELEEDGVHCSDMDECS-FSEFLC 233
 ||: ||:|||| | | | | ||: | | ||: || | | ||: ||: ||: : ||
 Db 973 ADGKHCEDVNECETRR-CSQECANIYGSYQCYCRQGYQLAEDGHTCTDIDECAQGAGILC 1031
 Qy 234 QHECVNQPGTYFCSCP-PGYILLDDNRSCQDINECEHRNHTCNLQQTCTYNLQGGFKCIDP 292
 ||| ||: | ||: || | : : |||: ||: || | : ||: ||: || | : ||
 Db 1032 TFRCVNVPGSYQCACPEQGYTMMANGRSCKDLDECALGTHNCSEAETCHNIQGSFRCL-R 1090
 Qy 293 IRCEEPYLRISDNRCMCPAENPGCRD-----QPFTILYRDMDVVSGRSVPADIFQMQAT 346
 | | : ||: | : | | : | | | : : | | ||| ||: ||
 Db 1091 FDCPPNYVRVSQTKC----ERTTCQDITECQTSPARITHYQLNFQTGLLVPAHIFRIGPA 1146
 Qy 347 TRYPGAYYIFQIKSGNEGREFYMRQTGPISATLVMTRPIKGPRIQLDLEM 397
 : | | | | | | : : : | : ||: ||: ||
 Db 1147 PAFAGDTISLTITKGNEEGYFVTRRLNAYTGVVSLQRSVLEPRDFALDVEM 1197

RESULT 6

S34968

fibulin, splice form D precursor - mouse

N;Alternate names: basement-membrane protein BM-90; calcium-binding protein BM-90

C;Species: Mus musculus (house mouse)

C;Date: 10-Dec-1993 #sequence_revision 10-Nov-1995 #text_change 02-Aug-2002

C;Accession: S34968; S36441; S13814

R;Pan, T.C.; Kluge, M.; Zhang, R.Z.; Mayer, U.; Timpl, R.; Chu, M.L.

Eur. J. Biochem. 215, 733-740, 1993

A;Title: Sequence of extracellular mouse protein BM-90/fibulin and its calcium-dependent binding to other basement-membrane ligands.

A;Reference number: S34968; MUID:93358897; PMID:8354280

A;Accession: S34968

A;Molecule type: mRNA

A;Residues: 1-705 <PAN>

R;Pan, T.C.; Kluge, M.; Zhang, R.Z.; Mayer, U.; Timpl, R.; Chu, M.L.

submitted to the EMBL Data Library, January 1993

A;Description: Sequence of extracellular mouse protein BM-90/fibulin and its calcium-dependent binding to other basement membrane ligands.

A;Reference number: S36440

A;Accession: S36441

A;Molecule type: mRNA

A;Residues: 1-39, 'P', 41-705 <PAW>

A;Cross-references: EMBL:X70854; NID:g396820; PIDN:CAA50207.1; PID:g396821

A;Experimental source: cell-line F9 teratocarcinoma

R;Kluge, M.; Mann, K.; Dziadek, M.; Timpl, R.

Eur. J. Biochem. 193, 651-659, 1990

A;Title: Characterization of a novel calcium-binding 90-kDa glycoprotein (BM-90) shared by basement membranes and serum.

A;Reference number: S13814; MUID:91065369; PMID:2249686

A;Accession: S13814

A;Molecule type: protein

A;Residues: 28;31-49, 'X', 51-53; 'XX', 110-117; 231-240, 'X', 242-243; 339-362, 'S', 364-387; 434-439; 469-476; 'Q', 554-557, 'Q', 559-563; 574-581 <KLU>

C;Superfamily: fibulin-1; EGF homology

C;Keywords: alternative splicing; basement membrane; calcium binding; extracellular matrix; glycoprotein; plasma

F;1-29/Domain: signal sequence #status predicted <SIG>
F;30-705/Product: fibulin, splice form D #status predicted <MAT>
F;98,537,541/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 29.2%; Score 702; DB 2; Length 705;
Best Local Similarity 35.2%; Pred. No. 5.4e-39;
Matches 160; Conservative 66; Mismatches 154; Indels 74; Gaps 21;

Qy	1	QCTNGFDLDRQSGQCLDIDECRTIPEACRGDMCMCVNQGGLYLCIPRTNPVYRGPYSNPYS	60
		: : : : :	
Db	295	QCKSGFIQD-ALGNCIDINECLSIAPCPVGQTCINTEGSYTC-----	336
Qy	61	TPYSGPYPAAPPLSAPNYPTISRPLICRFGYQM-DESNQCVDVDECATDSHQCNPTQIC	119
		: : : : :	
Db	337	-----QKNVPN-----CGRGYHLNEEGTRCVDVDECAPPAEPCGKGHHHC	375
Qy	120	INTEGGYTCSCTDGYWL--LEGQCLDIDEC-RY--GYCQQLCANVPGSYSCTCNPGFTLN	174
		: : : : : : : : : : :	
Db	376	LNSPGSFRCECKAGFYFDGISRTCVDINECQRYPGRLCGHKCENTPGSFHCSCSAGFRLS	435
Qy	175	EDGRSCQDVNECATENPCVQTCVNTYGSFICRCDPGYELEE-DGVHCSMDDECSF--SEF	231
		: : : : : : :	
Db	436	VDGRSCEDVNEC-LNSPCSQECANVYGSYQCYCRRGYQLSDVDGVTCEDIDECALPTGGH	494
Qy	232	LCQHECVNQPGTYFCSCP-PGYILLDDNRSCQDINECEHRNHTCNLQQTCYNLQGGFKCI	290
		: : : : : : : : : : : : : :	
Db	495	ICSYRCINIPGSFQCSCPSSGYRLAPNGRNCQDIDECVTGIHNCSINETCFNIQGSFRCL	554
Qy	291	DPIRCEEPYLRI SDN-----RCM--CPAENPGC-RDQPFTILYRDMDVVSGRSV--	336
		: : : : : : : :	
Db	555	S-FECPENYRRSADTFRQEKTDTVRCIKSCRPNDEACVRDPVHTVSHTVISLPTFREFT	613
Qy	337	PADIFQMATT-RYPG--AYYIFQIKSGNEGREFYM---RQTGPISATLVMTRPIKGP	390
		: : : : : :	
Db	614	PEEIIFLRAVTPLYPANQADIIFDITEGNLRDSFDIIKRYEDGMTVGVRQVRPIVGPFY	673
Qy	391	IQLDLEM-ITVNTVINFRGSSVIRLRIYVSQYPF	423
		: : : : : : :	
Db	674	AVLKLEMNYVLGGVVSHR--NVNVVHIFVSEYWF	705

RESULT 7

A55184

fibulin-2 precursor - human

N;Alternate names: protein DKFZp586A1519.1

C;Species: Homo sapiens (man)

C;Date: 27-Jan-1995 #sequence_revision 27-Jan-1995 #text change 08-Sep-2002

C;Accession: A55184; T08744

R; Zhang, R.Z.; Pan, T.C.; Zhang, Z.Y.; Mattei, M.G.; Timpl, R.; Chu, M.L.

Genomics 22, 425-430, 1994

A;Title: Fibulin-2 (FBLN2): human cDNA sequence, mRNA expression, and mapping of the gene on human and mouse chromosomes.

A;Reference number: A55184; MUID:95104855; PMID:7806230

A;Accession: A55184

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-1184 <ZHA>

A;Cross-references: GB:X82494; NID:g575232; PIDN:CAA57876.1; PID:g575233
 R;Wambutt, R.; Heubner, D.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S.
 submitted to the Protein Sequence Database, March 1999
 A;Reference number: Z16471
 A;Accession: T08744
 A;Molecule type: mRNA
 A;Residues: 656-719, 'QDECLMGAHDCSRRQFCVNTLGSFYCVNHTVLCADGYILNAHRKCVD', 720-
 853, 'T', 855-1184 <WAM>
 A;Cross-references: EMBL:AL050095
 A;Experimental source: adult uterus; clone DKFZp586A1519
 C;Genetics:
 A;Gene: GDB:FBLN2
 A;Cross-references: GDB:293037; OMIM:135821
 A;Map position: 3p25-3p24
 A;Note: DKFZp586A1519.1
 C;Superfamily: fibulin-2; EGF homology; von Willebrand factor type C repeat
 homology
 C;Keywords: alternative splicing; extracellular matrix
 F;1-27/Domain: signal sequence #status predicted <SIG>
 F;28-1184/Product: fibulin-2 protein #status predicted <MAT>
 F;905-941/Domain: EGF homology <EGF>

Query Match 29.1%; Score 701.5; DB 2; Length 1184;
 Best Local Similarity 34.5%; Pred. No. 9.1e-39;
 Matches 142; Conservative 58; Mismatches 152; Indels 59; Gaps 11;

```

Qy      1 QCTNGFDLDRQSGQCLDI DECRTI PEACRGDMMCVNQNGGYLCI PRTNPVYRGYPYSNPYS 60.
      :| :|| | | :|:|:| | :| | | | | |
Db      795 RCMDGF-LQDPEGNCVDINECTSLSEPCRPGFSCINTVGSYTC----- 836

Qy      61 TPYSGPYPAAPPLSAPNYPTISRPLICRFGYQ-MDESNQCVDVDECATDSHQCNPTQIC 119
      ||| | | | :| :|:|:| | | | | | |
Db      837 -----QRNPLICARGYHASDDGAKCVDVNECETGVHRCGEGQVC 875

Qy      120 INTEGgyTCsCTDgyw--LLEGQCLDI DECRYG---YCQQLCANVPGSYSCTCNPGFTLN 174
      | | | | | | :| :|:|:| | | | | | |
Db      876 HNLPGSYRCDCKAGFQRDAFGRGCIDVNECWASPGRLCQHTCENTLGSYRCSASGFLLA 935

Qy      175 EDGRSCQDVNECATENPCVQTCVNTYGSFICRCDPGYELEEDGVHCSDMDECS-FSEFLC 233
      ||: |:|:| | | :| | | | | | | | | | | |
Db      936 ADGKRCEdVNECEAQR-CSQECANIYGSYQCYCRQGYQLAEDGHTCTDIDECAQGAGILC 994

Qy      234 QHECVNQPGTYFCSCP-PGYILLDDNRSCQDINECEHRNHTCNLQQTCYNLQGGFKCIDP 292
      |:| |:|:| |:| | | :| :|:|:|:| | | :|:|:|:| |:|:|
Db      995 TFRCLNVPGSYQCACPEQGYTMTANGRSCKDVDECALGTHNCSEAETCHNIQGSFRCL-R 1053

Qy      293 IRCEEPYLRISDNRCMCPAENPGCRD-----QPFTILYRDMDVVSGRSVPADIFQMQAT 346
      | | |:|:| :| | | | | | | | :| :|:|:| | | | |:|
Db      1054 FECPPNYVQVSKTKC----ERTTCHDFLEcQNSPARITHYQLNFQTGLLVPAHIFRIGPA 1109

Qy      347 TRYPGAYYIFQIKSGNEGREFYMRQTGPISATLVMTRPIKGPREIQLDLEM 397
      :| | | | | | | :| :|:|:|:| | | | | | |
Db      1110 PAFTGDTIALNI IKNEEGYFGTRRLNAYTGvvYLQRAVLEPRDFALDDEM 1160

```

fibulin 1 precursor, splice form B - human
 C;Species: Homo sapiens (man)
 C;Date: 19-Apr-1991 #sequence_revision 19-Apr-1991 #text_change 02-Aug-2002
 C;Accession: B36346
 R;Argaves, W.S.; Tran, H.; Burgess, W.H.; Dickerson, K.
 J. Cell Biol. 111, 3155-3164, 1990
 A;Title: Fibulin is an extracellular matrix and plasma glycoprotein with
 repeated domain structure.
 A;Reference number: A36346; MUID:91100426; PMID:2269669
 A;Accession: B36346
 A;Molecule type: mRNA
 A;Residues: 1-601 <ARG>
 A;Cross-references: GB:X53742; NID:g31416; PIDN:CAA37771.1; PID:g31417
 C;Genetics:
 A;Gene: GDB:FBLN1; FBLN
 A;Cross-references: GDB:278285; OMIM:135820
 A;Map position: 22q13.3-22q13.3
 C;Superfamily: fibulin-1; EGF homology
 C;Keywords: alternative splicing
 F;180-214/Domain: EGF homology <EGF1>
 F;485-523/Domain: EGF homology <EGF>

Query Match 25.7%; Score 617.5; DB 2; Length 601;
 Best Local Similarity 38.3%; Pred. No. 1.7e-33;
 Matches 119; Conservative 46; Mismatches 95; Indels 51; Gaps 12;

```

Qy      1 QCTNGFDLDRQSGQCLDIDECRTIPEACRGDMMCVNQNGGYLCIPRTNPVYRGYPYNSNPYS 60
      || :|| | | :||| :| | | :| | |
Db      293 QCKSGFIQD-ALGNCIDINECLSISAPCPIGHTCINTEGSYTC----- 334

Qy      61 TPYSGPYPAAPPLSAPNYPTISRPLICRFGYQM-DESNQCVDVDECATDSHCNPTQIC 119
      : || | || :| :||| ||| : | |
Db      335 -----QKNVPN-----CGRGYHLNEEGTRCVDVDECAPPAEPCGKGHRC 373

Qy      120 INTEGGYTCSTDGYWL--LEGQCLDIDEC-RY--GYCQQLCANVPGSYSCTCNPGFTLN 174
      :| : | | || : | :||| || | | | ||| :| :| | :
Db      374 VNSPGSFRCECKTGYYFDGISRMCVDVNECQRYPGRLCGHKCENTLGSYLCSVGFRLS 433

Qy      175 EDGRSCQDVNECATENPCVQTCVNTYGSFICRCDPGYELEE-DGVHCSMDDECSF--SEF 231
      ||||| :| :||| :| || | | ||| :| | ||| :| ||| :
Db      434 VDGRSCEDINECSS-SPCSQECANVYGSYQCYCRRGYQLSDVDGVTCEDIDECALPTGGH 492

Qy      232 LCQHECVNQPGTYFCSCP-PGYILLDDNRSCQDINECEHRNHTCNLQQTTCYNLQGGFKCI 290
      :| : | :| ||| || | : | :||| :| | ||| :| :| :
Db      493 ICSYRCINIPGSFQCSCPSSGYRLAPNGRNCQDIDECVTGIHNCSINETCFNIQGAFRCL 552

Qy      291 DPIRCEEPYLR 301
      | | | |
Db      553 -AFECPENYRR 562

```

RESULT 9

T42760

fibulin, splice form D precursor - Caenorhabditis elegans

C;Species: Caenorhabditis elegans

C;Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 23-Sep-2002

C;Accession: T42760

R;Barth, J.L.; Argraves, K.M.; Roark, E.F.; Little, C.D.; Argraves, W.S.
submitted to the EMBL Data Library, February 1998

A;Description: Isolation of chicken and nematode fibulin-1 homologs and
characterization of the nematode fibulin-1 gene.

A;Reference number: Z22267

A;Accession: T42760

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: mRNA

A;Residues: 1-689 <BAR>

A;Cross-references: EMBL:AF051401; PIDN:AAC28321.1

C;Genetics:

A;Note: FBLN1

Query Match 25.1%; Score 603; DB 2; Length 689;
Best Local Similarity 27.4%; Pred. No. 1.7e-32;
Matches 156; Conservative 52; Mismatches 155; Indels 206; Gaps 19;

```
Qy      2 CTNGFDLDRQSGQCLDIDECRTIPEACRGDMMCVCNQNNGGYLCIPRTNPVYRGPYSNPYST 61
      | : ||| | | : ||| | | : : | : | | : | |
Db     180 CRSGFDLAPDGMACVDIDECATLMDDCLESQRCLNTPGSFKCI----- 222

Qy      62 PYSGPYPAAPPLSAPNYPTISRPLICRFGYQMD-ESNQCVDVDECATDSHQCNPTQICI 120
      | | | | | | | : : | | | | | | | | |
Db     223 -----RTLSCGTGYAMDSETERCRDVDECNLGSHDCGPLYQCR 260

Qy     121 NTEGGYTC-----SCTDGYWLLEGQCLDIDECRYGY----- 151
      ||:| | | : | : ||: | | | | | | :
Db     261 NTQGSYRCDAKKCGDGELQNPMTGECTSITCPNGYYPKNGMCNDIDECVTGHNCGAGEEC 320

Qy     152 -----CQQ---LCA-----NVPGSYSCTCNPGF 171
      ||| ||| | : ||: | | | | :
Db     321 VNTPGSFRCQQKGNLCAHGYEVNGATGFCEDVNECQQGVCGSMECINLPPTYKCKCGPGY 380

Qy     172 TLNE-----DGRSCQDVNECA 187
      | : | | | | | | | | | |
Db     381 EFNDAKKRCEDVDECIKFAGHVCDLSAECINTIGSFECKCKPGFQLASDGRRCEDVNECT 440

Qy     188 TE-NPCVQTCVNTYGSFICRCDPGYELEEDGVHCSMDDECSF----SEFLCQHECVNQPG 242
      | | | | | | : | | | : | | | | : | | | | | | | |
Db     441 TGIAACEQKCVNIPGSYQCICDRGFALGPDGTKCEDIDECSIWAGSGNDLCMGGCINTKG 500

Qy     243 TYFCSCPPGYILLDDNRSCQDINECEHRNHTCNLQQTTCYNLQGGFKCIDPIRCEEPYLRI 302
      : | | | | | : | | : | : | : | | | | | | | :
Db     501 SYLCQCPPGYKIQPDGRTCVDVDECA-MGECAGSDKVCVNTLGSKFC-HSIDCPTNYIHD 558

Qy     303 SDNR-----C--MCPAENPGC-RDQPFTILYRDMDVVSGRSV--PADI----- 340
      | | : | : | : | : | : | : | : | :
Db     559 SLNKNQIADGYSCIKVCSTEDTECLGNHTREVLYQFRAVPSLKTIIISPIEVSRIVTHMGV 618

Qy     341 -FQMQATTRYPGAYYIFQIKSGNEGREFYMRQTGPISATLVMTRPIKGPRIQLDLEMIT 399
      | : | | : : | | : : | | | : | |
Db     619 PFSVDYNLDYVGQRHFRIVQERNIG-----IVQLVKPISGP-----TVETIK 660

Qy     400 VNTVINFRGSSVIR-----LRIYVSQYPF 423
      || | | : : | | | | |
Db     661 VNIHTKSRTGVILAFNEAIIIEISVSKYPF 689
```

RESULT 10

T42990

fibulin 1, splice form C precursor - *Caenorhabditis elegans*

C;Species: *Caenorhabditis elegans*

C;Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 08-Sep-2002

C;Accession: T42990

R;Barth, J.L.; Argraves, K.M.; Roark, E.F.; Little, C.D.; Argraves, W.S.
submitted to the EMBL Data Library, February 1998

A;Description: Isolation of chicken and nematode fibulin-1 homologs and
characterization of the nematode fibulin-1 gene.

A;Reference number: Z22267

A;Accession: T42990

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: mRNA

A;Residues: 1-712 <BAR>

A;Cross-references: EMBL:AF051402; PIDN:AAC28322.1

C;Genetics:

A;Gene: FBLN1

C;Superfamily: fibulin-1; EGF homology

C;Keywords: alternative splicing; basement membrane; extracellular matrix

Query Match 24.8%; Score 596; DB 2; Length 712;
Best Local Similarity 27.9%; Pred. No. 5.1e-32;
Matches 152; Conservative 46; Mismatches 145; Indels 202; Gaps 18;

```

Qy      2 CTNGFDLDRQSGQCLDIDECRTIPEACRGDMMCNVNQGGYLCIPRTNPVYRGPYSNPYST 61
      | : ||| | | : ||| | | : : | | : | | : ||
Db      180 CRSGFDLAPDGMACVDIDECATLMDDCLESQRCLNTPGSFKCI ----- 222

Qy      62 PYSGPYPAAPPLSAPNYPTISRPLICRFGYQMD-ESNQCVDVDECATDSHQCNPQTQICI 120
      | | | | | | | | | : : | | | | | | | | | |
Db      223 -----RTLSCGTGYAMDSETERCRDVDECNLGSHDCGPLYQCR 260

Qy      121 NTEGGYTC-----SCTDGYWLLEGQCLDIDECRYGY----- 151
      || : | | | | : | : || : | | | | | | :
Db      261 NTQGSYRCDAKKCGDGELQNPMTGECTSITCPNGYYPKNGMCNDIDECVTGHNCGAGEEC 320

Qy      152 -----CQQ---LCA-----NVPGSYSCTCNPGF 171
      || | | | | | | | | | | : || : | | | | :
Db      321 VNTPGSFRCQQKGNLCAHGYEVNGATGFCEDVNECQQGVCGSMECINLPGTYKCKCGPGY 380

Qy      172 TLNE-----DGRSCQDVNECA 187
      | : | | | | | | | | | | | | | | |
Db      381 EFNDAKKRCEDVDECIKFAGHVCDLSAECINTIGSFECKCKPGFQLASDGRRCEDVNECT 440

Qy      188 TE-NPCVQTCVNTYGSFICRCDPGYELEEDGVHCSMDDECSF----SEFLCQHECVNQPG 242
      | | | | | | | | : | | | : | | | | : || | | | |
Db      441 TGIAACEQKCVNIPGSYQCICDRGFALGPDGTKCEDIDECSEIWAGSGNDLCMGGCINTKG 500

Qy      243 TYFCSCPPGYILLDDNRSCQDINECEHRNHTCNLQQTCYNLQGGFKCIDPIRCEEPYLRI 302
      : | | | | | : | | : | : | | : | | | | | | :
Db      501 SYLCQCPPGYKIQPDGRTCDVDDECA-MGECAGSDKVCVNTLGSFKC-HSIDCPTNYIHD 558

Qy      303 SDNR-----CMCPAENPGCRDQPFITILYRDMDVVSGRSVP----- 337
      | | : | | | | | | | : | : : : | : |
Db      559 SLNKNRCNRQPSACGLPEE---CSKVPLFLTYQFISL--ARAVPISSHRPAITLFKVSAP 613

```


Qy 338 --ADI---FQMQATTRYPGAYYIFQIKSGNEGREFYMRQTGP--ISATLVMTRPIKGP 390
 || |::| | || : |::| | | : : : ||:
 Db 614 NHADTEVNFELQLKTTIVGAPNVLP AIRAN-----FLLQKGEKRNSAVVTLRDSL DGPQT 668

Qy 391 IQLDL 395
 ::| |
 Db 669 VKLQL 673

RESULT 11

T43210

fibulin-1D precursor - *Caenorhabditis elegans* (fragment)

C;Species: *Caenorhabditis elegans*

C;Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 08-Sep-2002

C;Accession: T43210

R;Barth, J.L.; Argraves, K.M.; Roark, E.F.; Little, C.D.; Argraves, W.S.
 submitted to the EMBL Data Library, June 1998

A;Description: Identification of chicken and *C. elegans* fibulin-1 homologs and
 characterization of the *C. elegans* fibulin-1 gene.

A;Reference number: Z22337

A;Accession: T43210

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: DNA

A;Residues: 1-589 <BAR>

A;Cross-references: EMBL:AF070477; PIDN:AAC24035.1

C;Genetics:

A;Note: intron positions not resolved (incomplete sequence)

C;Superfamily: fibulin-1; EGF homology

Query Match 24.6%; Score 592.5; DB 2; Length 589;
 Best Local Similarity 27.4%; Pred. No. 7.4e-32;
 Matches 156; Conservative 52; Mismatches 155; Indels 207; Gaps 20;

Qy 2 CTNGFDLDRQSGQCLD-IDECRTIPEACRGDMMCVNQNGGYLCIPRTNPVYRGYPYNSNPYS 60
 | : ||| | : | ||| | : : | : | : | |
 Db 79 CRSGFDLAPDGMACVDHIDECATLMDDCLESQRCLNTPGSFKCI----- 122

Qy 61 TPYSGPYPAAPPLSAPNYPTISRPLICRFGYQMD-ESNQCVDVDECATDSHCNPTQIC 119
 | | | | | | : : | | | | | | | | | |
 Db 123 -----RTLSCGTGYAMDSETERCDVDECNLGSHDCGPLYQC 159

Qy 120 INTEGGYTC-----SCTDGYWLLEGQCLDIDECRYGY----- 151
 ||:| | | : | : ||: | | |||| | :
 Db 160 RNTQGSYRCDAKKCGDGELQNPMTGECTSITCPNGYYPKNGMCNDIDECVTGHNCGAGEE 219

Qy 152 -----CQQ---LCA-----NVPGSYSCTCNPG 170
 ||| ||| : ||:| | | | |
 Db 220 CVNTPGSFRCQQKGNLCAHGYEVNGATGFCEDVNECQQGVCGSMECINLPGTYKCKCGPG 279

Qy 171 FTLNE-----DGRSCQDVNEC 186
 : | : ||| | : |||| |
 Db 280 YEFNDAKKRCEDVDECIKFAGHVCDLSAECINTIGSFECKCKPGFQLASDGRRCEDVNEC 339

Qy 187 ATE-NPCVQTCVNITYGSFICRCDPGYELEDGVHCSMDDECSF-----SEFLCQHECVNQP 241
 | | | | | : | | | : | | | : ||| | | : |
 Db 340 TTGIAACEQKCVNIPGSYQCICDRGFALGPDGTKCEDIDECSIWAGSGNDLCMGGCINTK 399

```

Qy      242 GTYFCSCPPGYILLDDNRSCQDINECEHRNHTCNLQOTCYNLQGGFKCIDPIRCEEPYLR 301
      | : | | | | | : | | : | | : | | : | | | | | | | :
Db      400 GSYLCQCPPGYKIQPDGRTCDVDVDECA-MGECAGSDKVCVNTLGSKFC-HSIDCPTNYIH 457

Qy      302 ISDNR-----C--MCPAENPGC-RDQPFTILYRDMDVVSGRSV--PADI----- 340
      | | : | : | | : | : | | : | | : | : | : | :
Db      458 DSLNKNQIADGYSCIKVCSTEDTECLGNHTREVLYQFRAVPSLKTII SPIEVSRIVTHMG 517

Qy      341 --FQMQATTRYPGAYYIFQIKSGNEGREFYMRQTGPISATLVMTRPIKGPRIQLDLEMI 398
      | : | | : : | | : : : | | | : | |
Db      518 VPFSVDYNLDYVGQRHFRIVQERNIG-----IVQLVKPISGP-----TVETI 559

Qy      399 TVNTVINFRGSSVIR-----LRIYVSQYPF 423
      | | | | : : | | | | |
Db      560 KVNHTKSRTGVILAFNEAII EISVSKYPF 589

```

RESULT 12

T22793

hypothetical protein F56H11.1 - *Caenorhabditis elegans*

C;Species: *Caenorhabditis elegans*

C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 02-Aug-2002

C;Accession: T22793; T24489

R;Wilkinson, J.

submitted to the EMBL Data Library, January 1996

A;Reference number: Z19616

A;Accession: T22793

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: DNA

A;Residues: 1-798 <WIL>

A;Cross-references: EMBL:Z68749; PIDN:CAA92962.1; GSPDB:GN00022; CESP:F56H11.1

A;Experimental source: clone F56H11

R;Lloyd, C.

submitted to the EMBL Data Library, December 1995

A;Reference number: Z19897

A;Accession: T24489

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: DNA

A;Residues: 1-798 <WI2>

A;Cross-references: EMBL:Z68219; PIDN:CAA92483.1; GSPDB:GN00022; CESP:F56H11.1

A;Experimental source: clone T05A1

C;Genetics:

A;Gene: CESP:F56H11.1

A;Map position: 4

A;Introns: 14/1; 92/3; 144/1; 195/1; 281/1; 325/2; 371/2; 390/1; 437/1; 471/3;
498/3; 607/1; 649/2; 718/1

C;Superfamily: fibulin-1; EGF homology

Query Match 23.8%; Score 574; DB 2; Length 798;

Best Local Similarity 26.8%; Pred. No. 1.6e-30;

Matches 159; Conservative 49; Mismatches 172; Indels 214; Gaps 22;

```

Qy      2 CTNGFDLDRQSGQCLDI DECRTIPEACRGDMMCVNQNGGYLC-----IP---RTNPVY 51
      | : | | | | | | : | | | | | | | | | | | | : | | :
Db      180 CRSGFDLAPDGMACVDRNECLTRQSPCTQSEDCVNTIGGYICQRRISRLVPHRHRANRIG 239

```

```

Qy      52 RGP---YSNPYSTPYSGPYAAAPP----- 73
      |      :|||      :| | | :
Db      240 NAPRRMRDDPYSR--AGEYREASQANTEFGCPMGWLFQHGHCVDIDECATLMDDCLESQR 297

Qy      74 -LSAPNYPTISRPLICRFGYQMD---ESNQC-----DVDECATDSHQC 113
      | : |      | | | | | | | | | | | | | | | | | |
Db      298 CLNTPGSFKCIRTLSCGTGYAMDSETERNNCFILNNTFNCKYFFVEDVDECNLGSHDC 357

Qy      114 NPTQICINTEGGYTCS----- 129
      | | | | : | | |
Db      358 GPLYQCRNTQGSYRCDAKKCGDGELQNPMTGEYIDECVTGHNCGAGEECVNTPGSFRCQQ 417

Qy      130 ----CTDGYWL--LEGQCLDIDECRYGYCQQL--CANVPGSYSCTCNPGFTLNE----- 175
      | | | : | | | : | | | : | | | : | | | : | | | :
Db      418 KGNLCAHGYEVNGATGFCEDVNECQQGVCGSMECINLPGTYKCKCGPGYEFNDAKKRCED 477

Qy      176 -----DGRSCQDVNECATE-NPCVQTCV 197
      | | | | : | | | | | | | | | | | | | |
Db      478 VDECIKFAGHVCDLSAECINTIGSFECKCKPGFQLASDGRRCEDVNECTTGIAACEQKCV 537

Qy      198 NTYGSFICRCDPGYELEEDGVHCSDMDECSF----SEFLCQHECVNQPGTYFCSCPPGYI 253
      | | | : | | | : | | | | | | | | | | | | | | | |
Db      538 NIPGSYQICIDRGFALGPDGTKCEDIDEC SIWAGSGNDLCMGGCINTKGSYLCQCPPGYK 597

Qy      254 LLDDNRSCQDINECEHRNHTCNLQQTTCYNLQGGFKCIDPIRCEEPYLRISDNR----- 306
      : | | | : | | | : | | | | | | | | | | | | : | |
Db      598 IQPDGRTCDVDVDECA-MGECAGSDKVCVNTLGSFKC-HSIDCPTNYIHDSLKNKNCNRQP 655

Qy      307 --CMCPAENPGCRDQPFTILYRDMDVVSGRSVP-----ADI---FQM 343
      | | | | | | : | : : : | : | | | | | | | | | |
Db      656 SACGLPEE---CSKVPLFLTYQFISL--ARAVPISSHRPAITLFKVSAPNHADTEVN FEL 710

Qy      344 QATTRYPGAYYIFQIKSGNEGREFYMRQTGP--ISATLVMTRPIKGPRIQLDL 395
      | | | | : | | | : | | | | | | | | | | | | : | |
Db      711 QLKTTIVGAPNVLPAIRAN-----FLLQKGEKRNSAVVTLRDSLDGPQTVKLQL 759

```

RESULT 13

A35626

transforming growth factor beta-1-binding protein - human

C;Species: Homo sapiens (man)

C;Date: 21-Sep-1990 #sequence_revision 21-Sep-1990 #text_change 11-Jan-2000

C;Accession: A35626

R;Kanzaki, T.; Olofsson, A.; Moren, A.; Wernstedt, C.; Hellman, U.; Miyazono, K.; Claesson-Welsh, L.; Heldin, C.H.

Cell 61, 1051-1061, 1990

A;Title: TGF-beta1 binding protein: a component of the large latent complex of TGF-beta1 with multiple repeat sequences.

A;Reference number: A35626; MUID:90275601; PMID:2350783

A;Accession: A35626

A;Status: preliminary; not compared with conceptual translation

A;Molecule type: mRNA

A;Residues: 1-1394 <KAN>

A;Cross-references: GB:M34057; NID:g339547; PIDN:AAA61160.1; PID:g339548

C;Superfamily: unassigned EGF-related proteins; EGF homology

C;Keywords: alternative splicing

F;750-791/Domain: EGF homology <EGF>

Query Match 22.4%; Score 539; DB 2; Length 1394;
 Best Local Similarity 29.6%; Pred. No. 5.3e-28;
 Matches 126; Conservative 51; Mismatches 126; Indels 122; Gaps 17;

```

Qy      2 CTNGFDLDRQSGQCLDIDECRTIPEACRGDMMCVNQGGYLCI PRTNPVYRGPYSNPYST 61
      | | : | : | | | | : | | | : | |
Db      573 CYEGYRFSEQQRKCVDIDECTQVQHLC-SQGRCENTEGSF LCI----- 614

Qy      62 PYSGPYPAAPPLSAPNYPTISRPLI-----CRFGYQMDENQCVDVD 104
      : | : : : | : | | : | : | : |
Db      615 -CPAGFMASEEGTNCIDVDECLRPDVCGEHCVNTVGAFRCEYCDSGYRMTQGRCEDID 673

Qy      105 ECATDSHQCNPTQICINTEGGYTC-SCTDGYWLLEGQCLDIDEC-RYGYCQQ-LCANVPG 161
      | | | | : | : | | | | | : | : | | | | | | | | : | : |
Db      674 ECLNPS-TC-PDEQCVNSPGSYQCVPCTEGFRGWNGQCLDVDECLPNVCANGDCSNLEG 731

Qy      162 SYSCTCNPGFTLNEDGRSCQDVNECATENPCVQ----- 194
      | | | : | : | : | : | : | | | |
Db      732 SYMCSCHKGYTRTPDHKHCRDIDECQQGNLCVNGQCKNTEGSFRCTCGQGYQLSAAKDQC 791

Qy      195 -----TCVNTYGSFICRCDPGYELEEDGVHCSMDDECSFSEFLCQH-ECV 238
      | | | | | | | | | | | | : | : | : |
Db      792 EDIDECQHRHLCAHGQCRNTEGSFQCVCDQGYRASGLGDHCEINEDCLEDKSVCQRGDCI 851

Qy      239 NQPGTYFCSCPPGYILLDDNRSCQDINECEHRNHTCNLQQTCYNLQGGFKCI----- 290
      | | : | | : | | : | | | | | | | | | | | | : | : |
Db      852 NTAGSYDCTCPDGF-QLDDNKTCQDINECEHPG-LCGPQGECLNTEGSFHCVCQQGFSIS 909

Qy      291 -DPIRCEEPYLRI-----DN-----RCMC-----PAENPGCRDQPFTILYRDM 328
      | | | : : : | | | : | | | : |
Db      910 ADGRTCEDIDECVNNTVCDSHGFCDNTAGSFRCLCYQGFQAPQDQGQCV-----VNEC 963

Qy      329 DVVSG 333
      : : | |
Db      964 ELLSG 968
  
```

RESULT 14

A47221

fibrillin 1 precursor - human (fragment)

C;Species: Homo sapiens (man)

C;Date: 02-Jun-1995 #sequence_revision 25-Apr-1997 #text_change 02-Aug-2002

C;Accession: A47221; I54355; S17064; I59574; S17062; S62111; A34198

R;Corson, G.M.; Chalberg, S.C.; Dietz, H.C.; Charbonneau, N.L.; Sakai, L.Y.

Genomics 17, 476-484, 1993

A;Title: Fibrillin binds calcium and is coded by cDNAs that reveal a multidomain structure and alternatively spliced exons at the 5' end.

A;Reference number: A47221; MUID:94010947; PMID:7691719

A;Accession: A47221

A;Molecule type: mRNA

A;Residues: 1-337,'T',339-1029 <COR>

A;Cross-references: GB:X63556

R;Pereira, L.V.; D'Alessio, M.; Ramirez, F.; Lynch, J.; Sykes, B.; Pangilinan, T.; Bonadio, J.

Hum. Mol. Genet. 2, 961-968, 1993

A;Title: Genomic organization of the sequence coding for fibrillin, the defective gene product in Margan syndrome.
 A;Reference number: I54355; MUID:93372860; PMID:8364578
 A;Accession: I54355
 A;Status: preliminary; translated from GB/EMBL/DDBJ
 A;Molecule type: mRNA
 A;Residues: 132-3002 <PER>
 A;Cross-references: GB:L13923; NID:g306745; PIDN:AAB02036.1; PID:g306746
 R;Maslen, C.L.; Corson, G.M.; Maddox, B.K.; Glanville, R.W.; Sakai, L.Y. Nature 352, 334-337, 1991
 A;Title: Partial sequence of a candidate gene for the Marfan syndrome.
 A;Reference number: S17064; MUID:91304568; PMID:1852207
 A;Accession: S17064
 A;Molecule type: mRNA
 A;Residues: 1030-3002 <MAS>
 A;Cross-references: EMBL:X63556
 R;Dietz, H.C.; Valle, D.; Francomano, C.A.; Kendzior, R.J. Science 259, 680-683, 1993
 A;Title: The skipping of constitutive exons in vivo induced by nonsense mutations.
 A;Reference number: I59574; MUID:93157831; PMID:8430317
 A;Accession: I59574
 A;Status: preliminary; translated from GB/EMBL/DDBJ
 A;Molecule type: DNA
 A;Residues: 2217-2288,'I',2290-2325 <RES>
 A;Cross-references: GB:S54426; NID:g264860; PIDN:AAB25244.1; PID:g264861
 R;Lee, B.; Godfrey, M.; Vitale, E.; Hori, H.; Mattei, M.G.; Sarfarazi, M.; Tsipouras, P.; Ramirez, F.; Hollister, D.W. Nature 352, 330-334, 1991
 A;Title: Linkage of Marfan syndrome and a phenotypically related disorder to two different fibrillin genes.
 A;Reference number: S17062; MUID:91304567; PMID:1852206
 A;Accession: S17062
 A;Molecule type: mRNA
 A;Residues: 'VLVTVFIFLSYNKML',944-1444 <LEE1>
 A;Cross-references: EMBL:X62008; NID:g31398; PIDN:CAB56534.1; PID:g5924015
 A;Accession: S62111
 A;Molecule type: protein
 A;Residues: 1166-1176,'X',1178-1180,'D',1182-1185 <LEE2>
 R;Maddox, B.K.; Sakai, L.Y.; Keene, D.R.; Glanville, R.W. J. Biol. Chem. 264, 21381-21385, 1989
 A;Title: Connective tissue microfibrils. Isolation and characterization of three large pepsin-resistant domains of fibrillin.
 A;Reference number: A34198; MUID:90078246; PMID:2512293
 A;Accession: A34198
 A;Molecule type: protein
 A;Residues: 565-575;1890-1892,'I',1894-1900 <MAD>
 C;Comment: Fibrillin is a major component of elastin-associated microfibrils.
 C;Genetics:
 A;Gene: GDB:FBN1
 A;Cross-references: GDB:127115; OMIM:134797; OMIM:154700
 A;Map position: 15q21.1-15q21.1
 A;Introns: 2236/1; 2258/1; 2297/1
 C;Superfamily: fibrillin 1; EGF homology
 C;Keywords: alternative splicing; calcium binding; extracellular matrix; glycoprotein; Marfan syndrome

F;1-3002/Product: fibrillin (5'-region exon A splice form) (fragment) #status predicted <MATA>
 F;132-3002/Product: fibrillin (5'-region exon C splice form) #status predicted <MATC>
 F;1332-1367/Domain: EGF homology <EGF>
 F;1457-1492/Domain: EGF homology <EGF2>
 F;2262-2295/Domain: EGF homology <EGF1>

Query Match 21.7%; Score 523.5; DB 2; Length 3002;
 Best Local Similarity 30.3%; Pred. No. 1.1e-26;
 Matches 122; Conservative 47; Mismatches 120; Indels 113; Gaps 18;

```

Qy      1 QCTNGFDLDRQSGQCLDIDECRTIPEACRGDMMCVNQNGGYLCIPRTNPVYRGPYSNPYS 60
      :|:| | | : | | | | | | : | | | | | : : | :
Db      1185 RCDSGFALDSEERNCTDIDECRISPDLC-GRGQCVNTPGDFEC--KCDEGYESGF----- 1236

Qy      61 TPYSGPYPAAPPLSAPNYPTISR----PLICRF-----GYQMDSE-NQ 99
      : | | | | | | | | | | | | | | | | | | | | |
Db      1237 -----MMMKNCMDIDECQRDPLLCRGGVCHNTEGSYRCECPGHLSPNISA 1283

Qy      100 CVDVDECATDSHQCNPTQICINTEGGYTCSCTDGYWLLEGQ--CLDIDECRY--GYCQQL 155
      |:|:| | | :| | | | | | | | | | | | | | | | |
Db      1284 CIDINECELSAHLCPNGRCVNLIQKYQCACNPGYHSTPDRLFVCVDIDECSIMNGGCETF 1342

Qy      156 CANVPGSYSCTCNPGFTLNEDGRSCQDVNECATENP----- 191
      | | | | | | | | | | | | | | | | | | | | |
Db      1343 CTNSEGSYECSCQPGFALMPDQSRCTDIDEC-EDNPNICDGGQCTNIPGEYRCLCYDGM 1401

Qy      192 -----CVQ-----TCVNTYGSFICRCDPGYELEEDGVHCSMDDECSFSE 230
      || | | | | | | | | | | | | | | | | | | | |
Db      1402 ASEDMKTCVDVNECDLNPNICLSGTCENTKGSFICHCDMGYSGKKGKTGCTDINECEIGA 1461

Qy      231 FLC-QHE-CVNQPGTYFCSCPPGYILLDDNRSCQDINECEHRNHTCNLQQTTCYNLQGGFK 288
      | :| | | | | | | | | | | | | | | | | | | |
Db      1462 HNCCKHVACTNTAGSFKCSCSPGWI--GDGIKCTDLDECSNGTHMCSQHADCKNTMGSYR 1519

Qy      289 CIDPIRCEEPYL-----RISDNRCMCPAENPGCRDQP 320
      | : | | | | | | | | | | | | | | | | | | |
Db      1520 CL----CKEGYTGDFGTCTDLDECSNENLNL--GNGQCLNAP 1555

```

RESULT 15

A55567

fibrillin I - bovine

C;Species: Bos primigenius taurus (cattle)

C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 02-Aug-2002

C;Accession: A55567

R;Tilstra, D.J.; Li, L.; Potter, K.A.; Womack, J.; Byers, P.H.

Genomics 23, 480-485, 1994

A;Title: Sequence of the coding region of the bovine fibrillin cDNA and localization to bovine chromosome 10.

A;Reference number: A55567; MUID:95137597; PMID:7835900

A;Accession: A55567

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-2871 <TIL>

A;Cross-references: GB:L28748; NID:g508427; PIDN:AAA74122.1; PID:g508428

C;Superfamily: fibrillin 1; EGF homology
F;1201-1236/Domain: EGF homology <EGF>

Query Match 21.7%; Score 522.5; DB 2; Length 2871;
Best Local Similarity 29.9%; Pred. No. 1.2e-26;
Matches 120; Conservative 45; Mismatches 124; Indels 113; Gaps 16;

```
Qy      1 QCTNGFDLDRQSGQCLDIDECRTIPEACRGDMMCVNQNGGYLCIPRTNPVYRGPYSNPYS 60
      :| :|| || : | ||||| | : | | ||| | : | : : | :
Db      1054 RCDSGFALDSEERNCTDIDECRISPDLC-GRGQCVNTPGDFEC--KCDEGYESGF----- 1105

Qy      61 TPYSGPYPAAPPLSAPNYPTISR----PLICRFGYQMDSE-----NQ 99
      : | | | | | | | | | | | | | | | | | | | | | | | |
Db      1106 -----MMMKNCMDIDECQRDPLLCRGGVCLNTEGSYRCECPPGHQLAPNISA 1152

Qy      100 CVDVDECATDSHQCNPTQICINTEGGYTCSDTDGYWLLEGQ--CLDIDECRY--GYCQQL 155
      |:|::|| :| | | | :| | | | | | | | | | | | | | | |
Db      1153 CIDINECELSAHL- PHGRCVNLIGKYQCACNPGYHSTPDRLFCDVIDECSIMNGGCETF 1211

Qy      156 CANVPGSYSCTCNPGFTLNEDGRSCQDVNECATENP----- 191
      | | ||| |:| ||| | | ||| |::|| :||
Db      1212 CTNSEGSYECSCQPGFALMPDQRSDTDIDEC-EDNPNICDGGQCTNIPGEYRCLCYDGF 1270

Qy      192 -----CVQ-----TCVNTYGSFICRCDPGYELEEDGVHCSDMDECSFSE 230
      || | | | | | | | | | | | | | | | | | | | | | |
Db      1271 ASEDMKTCVDVNECDLNPNICLSGTCENTKGSFICHCDMGYSGKKGKTGCTDINECEIGA 1330

Qy      231 FLCQHE--CVNQPGTYFCSCPPGYILLDDNRSCQDINECEHRNHTCNLQOTCYNLQGGFK 288
      | | | | | | | | | | | | | | | | | | | | | | | |
Db      1331 HNCDRHAVCTNTAGSFKCSCSPGWI--GDGIKCTDLDECSNGTHMCSQHADCKNTMGSYR 1388

Qy      289 CIDPIRCEEPYL-----RISDNRCMCPAENPGCRDQP 320
      |: | | | | | | | | | | | | | | | | | | | | | |
Db      1389 CL----CKEGYTGDGFTCTDLDECSENLNLC--GNGQCLNAP 1424
```

Search completed: January 9, 2004, 12:34:54
Job time : 17.0264 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: January 9, 2004, 12:21:36 ; Search time 9.71297 Seconds
(without alignments)
2048.013 Million cell updates/sec

Title: US-09-674-379A-14
Perfect score: 2407
Sequence: 1 QCTNGFDLDRQSGQCLDIDE.....INFRGSSVIRLRIYVSQYPF 423

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_41:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	2407	100.0	448	1	FBL5_HUMAN	Q9ubx5 homo sapien
2	2303	95.7	448	1	FBL5_RAT	Q9wvh8 rattus norv
3	2302	95.6	448	1	FBL5_MOUSE	Q9wvh9 mus musculu
4	1276.5	53.0	443	1	FBL4_CRIGR	O55058 cricetulus
5	1276.5	53.0	443	1	FBL4_HUMAN	O95967 homo sapien
6	1272.5	52.9	443	1	FBL4_MOUSE	Q9wvj9 mus musculu
7	1108.5	46.1	493	1	FBL3_RAT	O35568 rattus norv
8	1093.5	45.4	493	1	FBL3_HUMAN	Q12805 homo sapien
9	729.5	30.3	1221	1	FBL2_MOUSE	P37889 mus musculu
10	721	30.0	598	1	FBL1_CERAE	Q8mjj9 cercopithec
11	713	29.6	704	1	FBL1_CHICK	O73775 gallus gall
12	701.5	29.1	1184	1	FBL2_HUMAN	P98095 homo sapien
13	700	29.1	703	1	FBL1_HUMAN	P23142 homo sapien
14	699	29.0	705	1	FBL1_MOUSE	Q08879 mus musculu
15	629.5	26.2	681	1	FBL1_BRARE	O42182 brachydanio
16	574	23.8	798	1	FBL1_CAEL	O77469 caenorhabdi
17	539	22.4	1394	1	LTBS_HUMAN	P22064 homo sapien

18	539	22.4	1595	1	LTBL_HUMAN	Q14766	homo sapien
19	523.5	21.7	2871	1	FBN1_HUMAN	P35555	homo sapien
20	522.5	21.7	2871	1	FBN1_BOVIN	P98133	bos taurus
21	518	21.5	1712	1	LTB1_RAT	Q00918	rattus norv
22	516.5	21.5	2871	1	FBN1_PIG	Q9tv36	sus scrofa
23	516	21.4	1389	1	LTBS_MOUSE	Q8cg18	mus musculu
24	516	21.4	1713	1	LTBL_MOUSE	Q8cg19	mus musculu
25	509.5	21.2	2871	1	FBN1_MOUSE	Q61554	mus musculu
26	509.5	21.2	2907	1	FBN2_MOUSE	Q61555	mus musculu
27	508.5	21.1	2911	1	FBN2_HUMAN	P35556	homo sapien
28	455	18.9	956	1	MTN2_HUMAN	O00339	homo sapien
29	431	17.9	956	1	MTN2_MOUSE	O08746	mus musculu
30	421	17.5	931	1	EMR1_MOUSE	Q61549	mus musculu
31	392	16.3	886	1	EMR1_HUMAN	Q14246	homo sapien
32	375	15.6	2470	1	NTC2_MOUSE	O35516	mus musculu
33	372	15.5	810	1	NEL1_HUMAN	Q92832	homo sapien
34	372	15.5	816	1	NEL2_MOUSE	Q61220	mus musculu
35	369	15.3	2471	1	NTC2_HUMAN	Q04721	homo sapien
36	367	15.2	2471	1	NTC2_RAT	Q9qw30	rattus norv
37	364	15.1	810	1	NEL1_RAT	Q62919	rattus norv
38	361.5	15.0	816	1	NEL2_HUMAN	Q99435	homo sapien
39	357.5	14.9	816	1	NEL2_RAT	Q62918	rattus norv
40	355.5	14.8	816	1	NEL_CHICK	Q90827	gallus gall
41	353.5	14.7	1964	1	NTC4_MOUSE	P31695	mus musculu
42	351.5	14.6	2437	1	NTC1_BRARE	P46530	brachydanio
43	350.5	14.6	652	1	CD93_HUMAN	Q9npy3	homo sapien
44	348.5	14.5	2703	1	NOTC_DROME	P07207	drosophila
45	347	14.4	644	1	CD93_MOUSE	O89103	mus musculu

ALIGNMENTS

RESULT 1

FBL5_HUMAN

ID FBL5_HUMAN STANDARD; PRT; 448 AA.

AC Q9UBX5; O75966;

DT 16-OCT-2001 (Rel. 40, Created)

DT 16-OCT-2001 (Rel. 40, Last sequence update)

DT 15-SEP-2003 (Rel. 42, Last annotation update)

DE Fibulin-5 precursor (FIBL-5) (Developmental arteries and neural crest

DE EGF-like protein) (Dance) (Urine p50 protein) (UP50).

GN FBLN5 OR DANCE.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=Melanoma;

RA Kostka G.;

RL Submitted (MAR-1999) to the EMBL/GenBank/DDBJ databases.

RN [2]

RP SEQUENCE FROM N.A.

RX MEDLINE=99357779; PubMed=10428823;

RA Nakamura T., Ruiz-Lozano P., Lindner V., Yabe D., Taniwaki M.,

RA Furukawa Y., Kobuke K., Tashiro K., Lu Z., Andon N.L., Schaub R.,

RA Matsumori A., Sasayama S., Chien K.R., Honjo T.;
 RT "DANCE, a novel secreted RGD protein expressed in developing,
 RT atherosclerotic, and balloon-injured arteries.";
 RL J. Biol. Chem. 274:22476-22483(1999).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Urine;
 RA Zemel R., Sholto O., Shaul Y.;
 RL Submitted (SEP-1998) to the EMBL/GenBank/DDBJ databases.
 CC -!- FUNCTION: PROMOTES ADHESION OF ENDOTHELIAL CELLS THROUGH
 CC INTERACTION OF INTEGRINS AND THE RGD MOTIF. COULD BE A VASCULAR
 CC LIGAND FOR INTEGRIN RECEPTORS AND MAY PLAY A ROLE IN VASCULAR
 CC DEVELOPMENT AND REMODELING.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- TISSUE SPECIFICITY: EXPRESSED PREDOMINANTLY IN HEART, OVARY, AND
 CC COLON BUT ALSO IN KIDNEY, PANCREAS, TESTIS, LUNG, AND PLACENTA.
 CC NOT DETECTABLE IN BRAIN, LIVER, THYMUS, PROSTATE, OR PERIPHERAL
 CC BLOOD LEUKOCYTES.
 CC -!- SIMILARITY: Belongs to the fibulin family.
 CC -!- SIMILARITY: Contains 6 EGF-like domains.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; AJ133490; CAB38568.1; -.
 DR EMBL; AF112152; AAD41768.1; -.
 DR EMBL; AF093118; AAC62107.1; -.
 DR HSSP; P00736; 1APQ.
 DR Genew; HGNC:3602; FBLN5.
 DR MIM; 604580; -.
 DR GO; GO:0005578; C:extracellular matrix; TAS.
 DR GO; GO:0005625; C:soluble fraction; TAS.
 DR GO; GO:0005178; F:integrin binding activity; TAS.
 DR GO; GO:0007160; P:cell-matrix adhesion; TAS.
 DR InterPro; IPR000152; Asx_hydroxyl.
 DR InterPro; IPR001881; EGF_Ca.
 DR InterPro; IPR006209; EGF_like.
 DR Pfam; PF00008; EGF; 4.
 DR SMART; SM00179; EGF_CA; 4.
 DR PROSITE; PS00010; ASX_HYDROXYL; 4.
 DR PROSITE; PS00022; EGF_1; FALSE_NEG.
 DR PROSITE; PS01186; EGF_2; 4.
 DR PROSITE; PS01187; EGF_CA; 6.
 KW Cell adhesion; Calcium-binding; Repeat; Signal; EGF-like domain;
 KW Glycoprotein.
 FT SIGNAL 1 23 POTENTIAL.
 FT CHAIN 24 448 FIBULIN-5.
 FT DOMAIN 24 69 EGF-LIKE 1, DIVERGENT.
 FT DOMAIN 127 167 EGF-LIKE 2, CALCIUM-BINDING (POTENTIAL).
 FT DOMAIN 168 206 EGF-LIKE 3, CALCIUM-BINDING (POTENTIAL).
 FT DOMAIN 207 246 EGF-LIKE 4, CALCIUM-BINDING (POTENTIAL).
 FT DOMAIN 247 287 EGF-LIKE 5, CALCIUM-BINDING (POTENTIAL).

FT	DOMAIN	288	333	EGF-LIKE 6, CALCIUM-BINDING (POTENTIAL).
FT	SITE	54	56	CELL ATTACHMENT SITE (POTENTIAL).
FT	DISULFID	131	144	BY SIMILARITY.
FT	DISULFID	138	153	BY SIMILARITY.
FT	DISULFID	155	166	BY SIMILARITY.
FT	DISULFID	172	181	BY SIMILARITY.
FT	DISULFID	177	190	BY SIMILARITY.
FT	DISULFID	192	205	BY SIMILARITY.
FT	DISULFID	211	221	BY SIMILARITY.
FT	DISULFID	217	230	BY SIMILARITY.
FT	DISULFID	232	245	BY SIMILARITY.
FT	DISULFID	251	262	BY SIMILARITY.
FT	DISULFID	258	271	BY SIMILARITY.
FT	DISULFID	273	286	BY SIMILARITY.
FT	DISULFID	292	305	BY SIMILARITY.
FT	DISULFID	299	314	BY SIMILARITY.
FT	DISULFID	320	332	BY SIMILARITY.
FT	CARBOHYD	283	283	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	296	296	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CONFLICT	69	70	IP -> HS (IN REF. 3).
FT	CONFLICT	147	148	TE -> MK (IN REF. 3).
SQ	SEQUENCE	448 AA;	50180 MW;	19FCA51FDA328003 CRC64;

Query Match 100.0%; Score 2407; DB 1; Length 448;
 Best Local Similarity 100.0%; Pred. No. 1.1e-171;
 Matches 423; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	QCTNGFDLDRQSGQCLDIDECRTIPEACRGDMMCVNQNGGYLCIPRTNPVYRGYPYNSNPYS	60
Db	26	QCTNGFDLDRQSGQCLDIDECRTIPEACRGDMMCVNQNGGYLCIPRTNPVYRGYPYNSNPYS	85
Qy	61	TPYSGPYPAAPPLSAPNYPTISRPLICRFGYQMDASNQCVDVDECATDSHQCNPQTQICI	120
Db	86	TPYSGPYPAAPPLSAPNYPTISRPLICRFGYQMDASNQCVDVDECATDSHQCNPQTQICI	145
Qy	121	NTEGGYTCSCTDGYWLLEGQCLDIDECRYGYCQQLCANVPGSYSCTCNPGFTLNEDGRSC	180
Db	146	NTEGGYTCSCTDGYWLLEGQCLDIDECRYGYCQQLCANVPGSYSCTCNPGFTLNEDGRSC	205
Qy	181	QDVNECATENPCVQTCVNTYGSFICRCDPGYELEEDGVHCSDMDECSFSEFLCQHECVNQ	240
Db	206	QDVNECATENPCVQTCVNTYGSFICRCDPGYELEEDGVHCSDMDECSFSEFLCQHECVNQ	265
Qy	241	PGTYFCSCPPGYILLDDNRSCQDINECEHRNHTCNLQQTCYNLQGGFKCIDPIRCEEPYL	300
Db	266	PGTYFCSCPPGYILLDDNRSCQDINECEHRNHTCNLQQTCYNLQGGFKCIDPIRCEEPYL	325
Qy	301	RISDNRCMCPAENPGCRDQPFTILYRDMDVVSGRSVPADIFQMQATTRYPGAYYIFQIKS	360
Db	326	RISDNRCMCPAENPGCRDQPFTILYRDMDVVSGRSVPADIFQMQATTRYPGAYYIFQIKS	385
Qy	361	GNEGREFYMRQTGPISATLVMTRPIKGPREIQLDLEMITVNTVINFRGSSVIRLRIYVSQ	420
Db	386	GNEGREFYMRQTGPISATLVMTRPIKGPREIQLDLEMITVNTVINFRGSSVIRLRIYVSQ	445
Qy	421	YPF	423

RESULT 2

FBL5_RAT

ID FBL5_RAT STANDARD; PRT; 448 AA.
AC Q9WVH8; Q9R284;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Fibulin-5 precursor (FIBL-5) (Developmental arteries and neural crest
DE EGF-like protein) (Dance) (Embryonic vascular EGF repeat-containing
DE protein) (EVEC).
GN FBLN5 OR DANCE.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99357779; PubMed=10428823;
RA Nakamura T., Ruiz-Lozano P., Lindner V., Yabe D., Taniwaki M.,
RA Furukawa Y., Kobuke K., Tashiro K., Lu Z., Andon N.L., Schaub R.,
RA Matsumori A., Sasayama S., Chien K.R., Honjo T.;
RT "DANCE, a novel secreted RGD protein expressed in developing,
RT atherosclerotic, and balloon-injured arteries.";
RL J. Biol. Chem. 274:22476-22483(1999).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=99278197; PubMed=10347091;
RA Kowal R.C., Richardson J.A., Miano J.M., Olson E.N.;
RT "EVEC, a novel epidermal growth factor-like repeat-containing protein
RT upregulated in embryonic and diseased adult vasculature.";
RL Circ. Res. 84:1166-1176(1999).
CC -!- FUNCTION: PROMOTES ADHESION OF ENDOTHELIAL CELLS THROUGH
CC INTERACTION OF INTEGRINS AND THE RGD MOTIF. COULD BE A VASCULAR
CC LIGAND FOR INTEGRIN RECEPTORS AND MAY PLAY A ROLE IN VASCULAR
CC DEVELOPMENT AND REMODELING.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: Belongs to the fibulin family.
CC -!- SIMILARITY: Contains 6 EGF-like domains.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; AF112153; AAD41769.1; -.
DR EMBL; AF137350; AAD25101.1; -.
DR HSSP; P00736; 1APQ.
DR InterPro; IPR000152; Asx_hydroxyl.
DR InterPro; IPR001881; EGF_Ca.
DR InterPro; IPR006209; EGF_like.
DR Pfam; PF00008; EGF; 4.

DR	SMART; SM00179; EGF_CA; 4.		
DR	PROSITE; PS00010; ASX_HYDROXYL; 4.		
DR	PROSITE; PS00022; EGF_1; FALSE_NEG.		
DR	PROSITE; PS01186; EGF_2; 4.		
DR	PROSITE; PS01187; EGF_CA; 6.		
KW	Cell adhesion; Calcium-binding; Repeat; Signal; EGF-like domain;		
KW	Glycoprotein.		
FT	SIGNAL	1	23
FT	CHAIN	24	448
FT	DOMAIN	24	69
FT	DOMAIN	127	167
FT	DOMAIN	168	206
FT	DOMAIN	207	246
FT	DOMAIN	247	287
FT	DOMAIN	288	333
FT	SITE	54	56
FT	DISULFID	131	144
FT	DISULFID	138	153
FT	DISULFID	155	166
FT	DISULFID	172	181
FT	DISULFID	177	190
FT	DISULFID	192	205
FT	DISULFID	211	221
FT	DISULFID	217	230
FT	DISULFID	232	245
FT	DISULFID	251	262
FT	DISULFID	258	271
FT	DISULFID	273	286
FT	DISULFID	292	305
FT	DISULFID	299	314
FT	DISULFID	320	332
FT	CARBOHYD	283	283
FT	CARBOHYD	296	296
FT	CONFLICT	238	238
SQ	SEQUENCE	448 AA;	50160 MW; E6BC68F7BF14B714CRC64;

```

      ||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||||
Db      266 PGSYFCSCPPGYVLLEDNRSCQDINECEHRNHTCTPLQTCYNLQGGFKCIDPIVCEEPYL 325

Qy      301 RISDNRCMCPAENPGCRDQPFTILYRDMDVVSGRSVPADIFQMQATTRYPGAYYIFQIKS 360
      | |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||
Db      326 LIGDNRCMCPAENTGCRDQPFTILFRDMDVVSGRSVPADIFQMQATTRYPGAYYIFQIKS 385

Qy      361 GNEGREFYMRQTGPISATLVMTRPIKGPRIQLDLEMITVNTVINFRGSSVIRLRIYVSQ 420
      |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||
Db      386 GNEGREFYMRQTGPISATLVMTRPIKGPRIQLDLEMITVNTVINFRGSSVIRLRIYVSQ 445

Qy      421 YPF 423
      |||
Db      446 YPF 448

```

RESULT 3

FBL5_MOUSE

```

ID      FBL5_MOUSE      STANDARD;      PRT;      448 AA.
AC      Q9WVH9;
DT      16-OCT-2001 (Rel. 40, Created)
DT      16-OCT-2001 (Rel. 40, Last sequence update)
DT      15-SEP-2003 (Rel. 42, Last annotation update)
DE      Fibulin-5 precursor (FIBL-5) (Developmental arteries and neural crest
DE      EGF-like protein) (Dance).
GN      FBLN5 OR DANCE.
OS      Mus musculus (Mouse).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX      NCBI_TaxID=10090;
RN      [1]
RP      SEQUENCE FROM N.A.
RX      MEDLINE=99357779; PubMed=10428823;
RA      Nakamura T., Ruiz-Lozano P., Lindner V., Yabe D., Taniwaki M.,
RA      Furukawa Y., Kobuke K., Tashiro K., Lu Z., Andon N.L., Schaub R.,
RA      Matsumori A., Sasayama S., Chien K.R., Honjo T.;
RT      "DANCE, a novel secreted RGD protein expressed in developing,
RT      atherosclerotic, and balloon-injured arteries.";
RL      J. Biol. Chem. 274:22476-22483(1999).
CC      -!- FUNCTION: PROMOTES ADHESION OF ENDOTHELIAL CELLS THROUGH
CC      INTERACTION OF INTEGRINS AND THE RGD MOTIF. COULD BE A VASCULAR
CC      LIGAND FOR INTEGRIN RECEPTORS AND MAY PLAY A ROLE IN VASCULAR
CC      DEVELOPMENT AND REMODELING.
CC      -!- SUBCELLULAR LOCATION: Secreted.
CC      -!- SIMILARITY: Belongs to the fibulin family.
CC      -!- SIMILARITY: Contains 6 EGF-like domains.
CC      -----
CC      This SWISS-PROT entry is copyright. It is produced through a collaboration
CC      between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC      the European Bioinformatics Institute. There are no restrictions on its
CC      use by non-profit institutions as long as its content is in no way
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CC      entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC      or send an email to license@isb-sib.ch).
CC      -----
DR      EMBL; AF112151; AAD41767.1; -.
DR      HSSP; P00736; 1APQ.

```

DR MGD; MGI:1346091; Fbln5.
 DR InterPro; IPR000152; Asx_hydroxyl.
 DR InterPro; IPR001881; EGF_Ca.
 DR InterPro; IPR006209; EGF_like.
 DR Pfam; PF00008; EGF; 4.
 DR SMART; SM00179; EGF_CA; 4.
 DR PROSITE; PS00010; ASX_HYDROXYL; 4.
 DR PROSITE; PS00022; EGF_1; FALSE_NEG.
 DR PROSITE; PS01186; EGF_2; 4.
 DR PROSITE; PS01187; EGF_CA; 6.
 KW Cell adhesion; Calcium-binding; Repeat; Signal; EGF-like domain;
 KW Glycoprotein.
 FT SIGNAL 1 23 POTENTIAL.
 FT CHAIN 24 448 FIBULIN-5.
 FT DOMAIN 24 69 EGF-LIKE 1, DIVERGENT.
 FT DOMAIN 127 167 EGF-LIKE 2, CALCIUM-BINDING (POTENTIAL).
 FT DOMAIN 168 206 EGF-LIKE 3, CALCIUM-BINDING (POTENTIAL).
 FT DOMAIN 207 246 EGF-LIKE 4, CALCIUM-BINDING (POTENTIAL).
 FT DOMAIN 247 287 EGF-LIKE 5, CALCIUM-BINDING (POTENTIAL).
 FT DOMAIN 288 333 EGF-LIKE 6, CALCIUM-BINDING (POTENTIAL).
 FT SITE 54 56 CELL ATTACHMENT SITE (POTENTIAL).
 FT DISULFID 131 144 BY SIMILARITY.
 FT DISULFID 138 153 BY SIMILARITY.
 FT DISULFID 155 166 BY SIMILARITY.
 FT DISULFID 172 181 BY SIMILARITY.
 FT DISULFID 177 190 BY SIMILARITY.
 FT DISULFID 192 205 BY SIMILARITY.
 FT DISULFID 211 221 BY SIMILARITY.
 FT DISULFID 217 230 BY SIMILARITY.
 FT DISULFID 232 245 BY SIMILARITY.
 FT DISULFID 251 262 BY SIMILARITY.
 FT DISULFID 258 271 BY SIMILARITY.
 FT DISULFID 273 286 BY SIMILARITY.
 FT DISULFID 292 305 BY SIMILARITY.
 FT DISULFID 299 314 BY SIMILARITY.
 FT DISULFID 320 332 BY SIMILARITY.
 FT CARBOHYD 283 283 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 296 296 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 448 AA; 50193 MW; F15CC70CCFBFDC97 CRC64;

Query Match 95.6%; Score 2302; DB 1; Length 448;
 Best Local Similarity 94.8%; Pred. No. 6.6e-164;
 Matches 401; Conservative 9; Mismatches 13; Indels 0; Gaps 0;

Qy 1 QCTNGFDLDRQSGQCLDIDECRTIPEACRGDMMCVNQNGGYLCIPRTNPVYRGYPYNSNPYS 60
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 26 QCTNGFDLDRQSGQCLDIDECRTIPEACRGDMMCVNQNGGYLCIPRTNPVYRGYPYNSNPYS 85
 Qy 61 TPYSGPYPAAPPLSAPNYPTISRPLICRFGYQMDESNQCVDVDECATDSHQCNPQTQICI 120
 | |||||||||: | |||||||: ||||||| ||||||||||||||||
 Db 86 TSYSGPYPAAPPVPASNYPTISRPLVCRFGYQMDEGNQCVDVDECATDSHQCNPQTQICI 145
 Qy 121 NTEGGYTCSCTDGYWLLEGQCLDIDECRYGYCQQLCANVPGSYSCTCNPGFTLNEDGRSC 180
 ||||||||||||||||||||||||||||||||||||||||||||: |||||
 Db 146 NTEGGYTCSCTDGYWLLEGQCLDIDECRYGYCQQLCANVPGSYSCTCNPGFTLNDDGRSC 205
 Qy 181 QDVNECATENPCVQTCVNTYGSFICRCDPGYELEEDGVHCSDMDECSFSEFLCQHECVNQ 240

Qy 241 PGTYFCSCPPGYILLDDNRSCQDINECEHRNHTCNLQOTCYNLQGGFKCIDPIRCEEPYL 300
 || : || || || || | ||||: || | : || | | ||::|| || |||:
 Db 262 PGRFSCCHCPQGYQLL-ATRLCQDIDECETGAHQCSAQTCVNFHGGYRCVDTNRCVEPYV 320

Qy 301 RISDNRCMCPAENPGCRDQPFTILYRDMDVVSGRSVPADIFQMQAATTRYPGAYYIFQIKS 360
 ::||| || || ||: || :||: | : | |||||: ||: |||: |||| |||:
 Db 321 QVSDNRCFCPVSNPLCREQPSSIVHRYMSITSESVPADVFQIQATSVPYGAYNAFQIRA 380

Qy 361 GNEGREFYMRQTGPISATLVMTRPIKGPREIQLDLEMITVNTVINFRGSSVIRLRIYVSQ 420
 || :||: || :|| ||: ||: |||| |||||: ||: ||::|| |||: || :||
 Db 381 GNTQGDYFIRQINNVSAMLVLARPVTPGREYVLDLEMTMNSLMSYRASSVLRLTVFVGA 440

Qy 421 YPF 423
 ||
 Db 441 YTF 443

RESULT 5

FBL4_HUMAN

ID FBL4_HUMAN STANDARD; PRT; 443 AA.
 AC O95967; O75967;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE EGF-containing fibulin-like extracellular matrix protein 2 precursor
 DE (Fibulin-4) (FIBL-4) (UPH1 protein).
 GN EFEMP2 OR FBLN4.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Melanoma;
 RX MEDLINE=20068041; PubMed=10601734;
 RA Giltay R., Timpl R., Kostka G.;
 RT "Sequence, recombinant expression and tissue localization of two novel
 RT extracellular matrix proteins, fibulin-3 and fibulin-4."
 RL Matrix Biol. 18:469-480(1999).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Zemel R., Shaul Y.;
 RL Submitted (SEP-1998) to the EMBL/GenBank/DDBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20435063; PubMed=10982184;
 RA Katsanis N., Venable S., Smith J.R., Lupski J.R.;
 RT "Isolation of a paralog of the Doyme honeycomb retinal dystrophy gene
 RT from the multiple retinopathy critical region on 11q13."
 RL Hum. Genet. 106:66-72(2000).
 RN [4]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RX MEDLINE=22388257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length
 RT human and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- SIMILARITY: Belongs to the fibulin family.
 CC -!- SIMILARITY: Contains 6 EGF-like domains.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; AJ132819; CAA10791.2; -.
 DR EMBL; AF093119; AAC62108.1; -.
 DR EMBL; AF109121; AAF65188.1; -.
 DR EMBL; BC010456; AAH10456.1; -.
 DR HSSP; P35555; 1EMN.
 DR Genew; HGNC:3219; EFEMP2.
 DR MIM; 604633; -.
 DR GO; GO:0005604; C:basement membrane; TAS.
 DR GO; GO:0005201; F:extracellular matrix structural constituent; TAS.
 DR InterPro; IPR000152; Asx_hydroxyl.
 DR InterPro; IPR001881; EGF_Ca.
 DR InterPro; IPR006209; EGF_like.
 DR InterPro; IPR001491; Thrbomoduln.
 DR Pfam; PF00008; EGF; 4.
 DR PRINTS; PR00907; THRMBOMODULN.
 DR SMART; SM00179; EGF_CA; 4.
 DR PROSITE; PS00010; ASX_HYDROXYL; 4.
 DR PROSITE; PS00022; EGF_1; FALSE_NEG.
 DR PROSITE; PS01186; EGF_2; 4.
 DR PROSITE; PS01187; EGF_CA; 6.
 KW Repeat; EGF-like domain; Calcium-binding; Glycoprotein; Signal.
 FT SIGNAL 1 25 POTENTIAL.
 FT CHAIN 26 443 EGF-CONTAINING FIBULIN-LIKE EXTRACELLULAR
 FT MATRIX PROTEIN 2.
 FT DOMAIN 36 81 EGF-LIKE 1, DIVERGENT.
 FT DOMAIN 123 163 EGF-LIKE 2, CALCIUM-BINDING (POTENTIAL).
 FT DOMAIN 164 202 EGF-LIKE 3, CALCIUM-BINDING (POTENTIAL).
 FT DOMAIN 203 242 EGF-LIKE 4, CALCIUM-BINDING (POTENTIAL).

FT	DOMAIN	243	282	EGF-LIKE 5, CALCIUM-BINDING (POTENTIAL).
FT	DOMAIN	283	328	EGF-LIKE 6, CALCIUM-BINDING (POTENTIAL).
FT	DISULFID	127	140	BY SIMILARITY.
FT	DISULFID	134	149	BY SIMILARITY.
FT	DISULFID	151	162	BY SIMILARITY.
FT	DISULFID	168	177	BY SIMILARITY.
FT	DISULFID	173	186	BY SIMILARITY.
FT	DISULFID	188	201	BY SIMILARITY.
FT	DISULFID	207	217	BY SIMILARITY.
FT	DISULFID	213	226	BY SIMILARITY.
FT	DISULFID	228	241	BY SIMILARITY.
FT	DISULFID	247	258	BY SIMILARITY.
FT	DISULFID	254	267	BY SIMILARITY.
FT	DISULFID	269	281	BY SIMILARITY.
FT	DISULFID	287	300	BY SIMILARITY.
FT	DISULFID	294	309	BY SIMILARITY.
FT	DISULFID	315	327	BY SIMILARITY.
FT	CARBOHYD	198	198	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	394	394	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CONFLICT	5	5	A -> T (IN REF. 1).
FT	CONFLICT	44	51	EWDPDSQH -> TQTAN (IN REF. 2).
FT	CONFLICT	103	111	AQHPNPCPP -> VNTQPLPT (IN REF. 2).
FT	CONFLICT	294	294	C -> W (IN REF. 2).
FT	CONFLICT	354	356	RSV -> AER (IN REF. 2).
FT	CONFLICT	355	355	S -> R (IN REF. 3).
SQ	SEQUENCE	443 AA;	49391 MW;	9E9AC2393780D3B8 CRC64;

Query Match 53.0%; Score 1276.5; DB 1; Length 443;
Best Local Similarity 52.0%; Pred. No. 8.4e-88;
Matches 220; Conservative 67; Mismatches 119; Indels 17; Gaps 4;

Qy	1	QCTNGFDLDRQSGQCLDIDECRTIPEACRGDMMCVNQNGGYLCIPRTNPVYRGPYSNPYS	60
Db	38	ECTDGYEWDPPDSQHCRDVNECLTIPEACKGEMKCINHYGGYLCLPRSAAVINDLHG----	93
Qy	61	TPYSGPYPAAPPLSAPNYPTISRPLICRFGYQMDESNQCVDVDECATDSHCNPTQICI	120
Db	94	---EGP-PPPVPFAQHFN-----PCPPGYEPDDQDSCVDVDECAQALHDCRPSQDCH	141
Qy	121	NTEGGYTCSCTDGYWLLEGQCLDIDECYGYCQQLCANVPGSYSCTCNPGFTLNEDGRSC	180
Db	142	NLPGSYQCTCPDGYRKIGPECVDIDECRYRYCQHRCVNLPGSFRCQCEPGFQLGPNNRSC	201
Qy	181	QDVNECATENPCVQTCVNTYGSFICRCDPGYELEEDGVHCSMDDECSFSEFLCQHECVNQ	240
Db	202	VDVNECDMGAPCEQRCFNSYGTFLCRCHQGELHRDGFSCSDIDECSYSSYLCQYRCVNE	261
Qy	241	PGTYFCSCPPGYILLDDNRSCQDINECEHRNHTCNLQOTCYNLQGGFKCIDPIRCEEPLY	300
Db	262	PGRFSCHCPQGYQLL-ATRLCQDIDECESGAHQCSAQTCNVFHGGYRCVDTNRCVEPYI	320
Qy	301	RISDNRCMCPAENPGCRDQPFTILYRDMDVVSGRSVPADIFQMQAATTRYPGAYYIFQIKS	360
Db	321	QVSENRLCLPASNPLCREQPSSI VHRYMTITSERSVPADV FQIQATSVPYGAYNAFQIRA	380
Qy	361	GNEGREFYMRQTGPISATLVMTMPIKGPREIQLDLEMITVNTVINFRGSSVIRLRIYVSQ	420

Db 381 GNSQGDFYIRQINNVSAMLVLARPVTGPREYVLDLEMVTMNSLMSYRASSVLRLTVFVGA 440

Qy 421 YPF 423

Db 441 YTF 443

RESULT 6

FBL4_MOUSE

ID FBL4_MOUSE STANDARD; PRT; 443 AA.

AC Q9WVJ9;

DT 16-OCT-2001 (Rel. 40, Created)

DT 16-OCT-2001 (Rel. 40, Last sequence update)

DT 15-SEP-2003 (Rel. 42, Last annotation update)

DE EGF-containing fibulin-like extracellular matrix protein 2 precursor

DE (Fibulin-4) (FIBL-4) (Mutant p53 binding protein 1).

GN EFEMP2 OR FBLN4 OR MBP1.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI_TaxID=10090;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=C57BL/6J;

RX MEDLINE=99308589; PubMed=10380882;

RA Gallagher W.M., Argentini M., Sierra V., Bracco L., Debussche L.,

RA Conseiller E.;

RT "MBP1: a novel mutant p53-specific protein partner with oncogenic

RT properties.";

RL Oncogene 18:3608-3616(1999).

CC -!- SUBUNIT: BINDS PREFERENTIALLY TO P53 MUTANTS.

CC -!- SUBCELLULAR LOCATION: Secreted.

CC -!- SIMILARITY: Belongs to the fibulin family.

CC -!- SIMILARITY: Contains 6 EGF-like domains.

CC -----

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CC -----

DR EMBL; AF104223; AAD45219.1; -.

DR HSSP; P00736; 1APQ.

DR MGD; MGI:1891209; Efemp2.

DR InterPro; IPR000152; Asx_hydroxyl.

DR InterPro; IPR001881; EGF_Ca.

DR InterPro; IPR006209; EGF_like.

DR InterPro; IPR001491; Thrbomoduln.

DR Pfam; PF00008; EGF; 4.

DR PRINTS; PR00907; THRMBOMODULN.

DR SMART; SM00179; EGF_CA; 4.

DR PROSITE; PS00010; ASX_HYDROXYL; 4.

DR PROSITE; PS00022; EGF_1; FALSE_NEG.

DR PROSITE; PS01186; EGF_2; 4.

DR PROSITE; PS01187; EGF_CA; 6.

KW Repeat; EGF-like domain; Calcium-binding; Glycoprotein; Signal.
 FT SIGNAL 1 25 POTENTIAL.
 FT CHAIN 26 443 EGF-CONTAINING FIBULIN-LIKE EXTRACELLULAR
 FT MATRIX PROTEIN 2.
 FT DOMAIN 36 81 EGF-LIKE 1, DIVERGENT.
 FT DOMAIN 123 163 EGF-LIKE 2, CALCIUM-BINDING (POTENTIAL).
 FT DOMAIN 164 202 EGF-LIKE 3, CALCIUM-BINDING (POTENTIAL).
 FT DOMAIN 203 242 EGF-LIKE 4, CALCIUM-BINDING (POTENTIAL).
 FT DOMAIN 243 282 EGF-LIKE 5, CALCIUM-BINDING (POTENTIAL).
 FT DOMAIN 283 328 EGF-LIKE 6, CALCIUM-BINDING (POTENTIAL).
 FT DISULFID 127 140 BY SIMILARITY.
 FT DISULFID 134 149 BY SIMILARITY.
 FT DISULFID 151 162 BY SIMILARITY.
 FT DISULFID 168 177 BY SIMILARITY.
 FT DISULFID 173 186 BY SIMILARITY.
 FT DISULFID 188 201 BY SIMILARITY.
 FT DISULFID 207 217 BY SIMILARITY.
 FT DISULFID 213 226 BY SIMILARITY.
 FT DISULFID 228 241 BY SIMILARITY.
 FT DISULFID 247 258 BY SIMILARITY.
 FT DISULFID 254 267 BY SIMILARITY.
 FT DISULFID 269 281 BY SIMILARITY.
 FT DISULFID 287 300 BY SIMILARITY.
 FT DISULFID 294 309 BY SIMILARITY.
 FT DISULFID 315 327 BY SIMILARITY.
 FT CARBOHYD 198 198 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 394 394 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 443 AA; 49425 MW; 4969C0328A23DD88 CRC64;

Query Match 52.9%; Score 1272.5; DB 1; Length 443;
 Best Local Similarity 52.0%; Pred. No. 1.7e-87;
 Matches 220; Conservative 65; Mismatches 121; Indels 17; Gaps 3;

Qy 1 QCTNGFDLDRQSGQCLDIDECRTIPEACRGDMMCVNQNGGYLCIPRTNPVYRGYPYSNPYS 60
 :||:|::| | | |::|| |||||:|:| |:| |||||:|:| | :
 Db 38 ECTDGYEWDADSQHCRDVNECLTIPEACKGEMKCNHYGGYLCIPRSAAVISDLHG---- 93
 Qy 61 TPYSGPYPAAPPLSAPNYPTISRPLICRFGYQMDENQCVDVDECATDSHCNPTQICI 120
 || | || :| | ||: || ||||| | | |:| |
 Db 94 ---EGPPPPAA-----HAQQPNPCPGYEPDEQESCVDVDECTQALHDCRPSQDCH 141
 Qy 121 NTEGGYTCSTDGYWLLEGQCLDIDECRYGYCQQLCANVPGSYSCNPGFTLNEDGRSC 180
 | | | |:| || | : |:| ||||| || | |:| |:| | | | | : |||
 Db 142 NLPGSYQCTCPDGYRKIGPECVDIDECRYRYCQHRCVNLPGSFRCQCEPGFQLGPNNRSC 201
 Qy 181 QDVNECATENPCVQTCVNTYGSFICRCDPGYELEEDGVHCSDMDECSFSEFLCQHECVNQ 240
 |||| | | | |:| |:| |:| |:| || | || |:| |:| |:| |:|
 Db 202 VDVNECDMGAPCEQRCFNSYGTFLCRCNQGYELHRDGFSCSDIDECGYSSYLCQYRCVNE 261
 Qy 241 PGTYFCSCPPGYILLDDNRSCQDINECEHRNHTCNLQQTTCYNLQGGFKCIDPIRCEEPYL 300
 || : | | | | | | | |||:| | | | | | | |:| |:| | | | |
 Db 262 PGRFSCHCPQGYQLL-ATRLCQDIDECETGAHQCEAQTTCVNFHGGYRCVDTNRCVEPYV 320
 Qy 301 RISDNRCMCPAENPGCRDQPFITILYRDMDVVSGRSVPADIFQMQATTRYPGAYYIFQIKS 360
 ::||| |:| | | | |:| |:| | : | | ||||| |:| |:| | ||| | |:|
 Db 321 QVSDNRCLCPASNPLCREQPSSIVHRYMSITERSVPADVFIQATSVPAYNAFQIRS 380

FT	SIGNAL	1	17	POTENTIAL.
FT	CHAIN	18	493	EGF-CONTAINING FIBULIN-LIKE EXTRACELLULAR
FT				MATRIX PROTEIN 1.
FT	DOMAIN	26	71	EGF-LIKE 1, DIVERGENT.
FT	DOMAIN	173	213	EGF-LIKE 2, CALCIUM-BINDING (POTENTIAL).
FT	DOMAIN	214	253	EGF-LIKE 3, CALCIUM-BINDING (POTENTIAL).
FT	DOMAIN	254	293	EGF-LIKE 4, CALCIUM-BINDING (POTENTIAL).
FT	DOMAIN	294	333	EGF-LIKE 5, CALCIUM-BINDING (POTENTIAL).
FT	DOMAIN	334	378	EGF-LIKE 6, CALCIUM-BINDING (POTENTIAL).
FT	DISULFID	177	190	BY SIMILARITY.
FT	DISULFID	184	199	BY SIMILARITY.
FT	DISULFID	201	212	BY SIMILARITY.
FT	DISULFID	218	228	BY SIMILARITY.
FT	DISULFID	224	237	BY SIMILARITY.
FT	DISULFID	239	252	BY SIMILARITY.
FT	DISULFID	258	268	BY SIMILARITY.
FT	DISULFID	264	277	BY SIMILARITY.
FT	DISULFID	279	292	BY SIMILARITY.
FT	DISULFID	298	309	BY SIMILARITY.
FT	DISULFID	305	318	BY SIMILARITY.
FT	DISULFID	320	332	BY SIMILARITY.
FT	DISULFID	338	350	BY SIMILARITY.
FT	DISULFID	344	359	BY SIMILARITY.
FT	DISULFID	365	377	BY SIMILARITY.
SQ	SEQUENCE	493 AA;	54596 MW;	22DAFD70BACF1CA5 CRC64;

Query Match 46.1%; Score 1108.5; DB 1; Length 493;
 Best Local Similarity 43.6%; Pred. No. 2.7e-75;
 Matches 204; Conservative 68; Mismatches 149; Indels 47; Gaps 5;

Qy	1	QCTNGFDLDRQSGQCLDIDECRTIPEACRGDMMCVNQNGGYLCIPRTNPVYRGYPYNSNPYS	60
		: : : : : :	
Db	28	QCTDGYEWDVPVRQQCKDIDECDIVPDAKGGMKCVNHYGGYLCPLPKTAQIIVNNEQPQQE	87
Qy	61	TPYS-----GYPYAAAPPLSAPNYPT-----	81
		: : : : : : :	
Db	88	TPAAEASSGAATGTIAARSMATSGVI PGGGFIASATAVAGPEVQTGRNNFVIRRNPA DPQ	147
Qy	82	-----ISRPLICRFGYQMDESNQCVDDVDECATDSHQCNPTQICINTEGGYTCSCTDGYWL	136
		: : : : : : : : :	
Db	148	RIPSNPSHRIQCAAGYEQSEHNVCQDIDECTSGTHNCRLDQVCINLRGSFTCHCLPGYQK	207
Qy	137	LEGQCLDIDECRY-GYCQQLCANVPGSYSCTCNPGFTLNEDGRSCQDVNECATENPCVQT	195
		: : : : : :	
Db	208	RGEQCVDIDECVPPYCHQGCVNTPGSFYCQCNPQGFQLAANNYTCVDINECDASNQCAQQ	267
Qy	196	CVNTYGSFICRCDPGYELEEDGVHCSMDDECSFSEFLCQHECVNQPGTYFCSCPPGYILL	255
		: : : : : : : : : :	
Db	268	CYNILGSFICQCNQGYELSSDRLNCEDIDECRTSSYLCQYQCVNEPGKFSCMCPQGYQVV	327
Qy	256	DDNRSCQDINECEHRNHTCNLQQTTCYNLQGGFKCIDPIRCEEPLYLRISDNRCMCPAENPG	315
		: : : : : : : : :	
Db	328	-RSRTCQDINECETTNE-CREDEMWNHYHGGFRCPQNPCQDPYVLTSENRCVCPVSN TM	385
Qy	316	CRDQPFTILYRDMDVVSGRSVPADIFQMQAATTRYPGAYYIFQIKSGNEGREFYMRQTGPI	375
		: : : : : : : :	
Db	386	CRDVPQSI VYKYMNI RSDRSVPSDIFQIQATTIYANTINTFRIKSGNENGFEYLRQTSPV	445

Qy 376 SATLVMTRPIKGPREIQLDLEMITVNTVINFRGSSVIRLRIYVSQYPF 423
 || ||: : : |||| : |||:|:|:| || |||:| | | : |
 Db 446 SAMLVLVKSLTGPREHIVGLEMLTVSSIGTFRTSSVLRLTIIVGPF SF 493

RESULT 8

FBL3_HUMAN

ID FBL3_HUMAN STANDARD; PRT; 493 AA.
 AC Q12805;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE EGF-containing fibulin-like extracellular matrix protein 1 precursor
 DE (Fibulin-3) (FIBL-3) (Fibrillin-like protein) (Extracellular protein
 DE S1-5).
 GN EFEMP1 OR FBLN3 OR FBNL.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A., AND POSSIBLE ALTERNATIVE SPLICING.
 RC TISSUE=Skin;
 RX MEDLINE=95097983; PubMed=7799918;
 RA Lecka-Czernik B., Lumpkin C.K. Jr., Goldstein S.;
 RT "An overexpressed gene transcript in senescent and quiescent human
 RT fibroblasts encoding a novel protein in the epidermal growth factor-
 RT like repeat family stimulates DNA synthesis.";
 RL Mol. Cell. Biol. 15:120-128(1995).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=97001163; PubMed=8812496;
 RA Ikegawa S., Toda T., Okui K., Nakamura Y.;
 RT "Structure and chromosomal assignment of the human S1-5 gene (FBNL)
 RT that is highly homologous to fibrillin.";
 RL Genomics 35:590-592(1996).
 RN [3]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20068041; PubMed=10601734;
 RA Giltay R., Timpl R., Kostka G.;
 RT "Sequence, recombinant expression and tissue localization of two novel
 RT extracellular matrix proteins, fibulin-3 and fibulin-4.";
 RL Matrix Biol. 18:469-480(1999).
 RN [4]
 RP VARIANT DHRD/MLVT TRP-345, AND VARIANT PHE-220.
 RX MEDLINE=99295941; PubMed=10369267;
 RA Stone E.M., Lotery A.J., Munier F.L., Heon E., Piguet B., Guymer R.H.,
 RA Vandenburgh K., Cousin P., Nishimura D., Swiderski R.E., Silvestri G.,
 RA Mackey D.A., Hagerman G.S., Bird A.C., Sheffield V.C.,
 RA Schorderet D.F.;
 RT "A single EFEMP1 mutation associated with both malattia Leventinese
 RT and Doyme honeycomb retinal dystrophy.";
 RL Nat. Genet. 22:199-202(1999).
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=4;

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CC      Comment=Experimental confirmation may be lacking for some
CC      isoforms;
CC      Name=1;
CC      IsoId=Q12805-1; Sequence=Displayed;
CC      Name=2;
CC      IsoId=Q12805-2; Sequence=VSP_001392;
CC      Name=3;
CC      IsoId=Q12805-3; Sequence=VSP_001393;
CC      Name=4;
CC      IsoId=Q12805-4; Sequence=VSP_001394;
CC      -!- DISEASE: DEFECTS IN EFEMP1 ARE A CAUSE OF DOYNE HONEYCOMB RETINAL
CC      DYSTROPHY (DHRD) ALSO KNOWN AS MALATTIA LEVENTINESE (MLVT OR ML),
CC      AN AUTOSOMAL DOMINANT DISEASE CHARACTERIZED BY YELLOW-WHITE
CC      DEPOSITS KNOWN AS DRUSEN THAT ACCUMULATE BENEATH THE RETINAL
CC      PIGMENT EPITHELIUM.
CC      -!- SIMILARITY: Belongs to the fibulin family.
CC      -!- SIMILARITY: Contains 6 EGF-like domains.
CC      -----
CC      This SWISS-PROT entry is copyright. It is produced through a collaboration
CC      between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC      the European Bioinformatics Institute. There are no restrictions on its
CC      use by non-profit institutions as long as its content is in no way
CC      modified and this statement is not removed. Usage by and for commercial
CC      entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC      or send an email to license@isb-sib.ch).
CC      -----
DR      EMBL; U03877; AAA65590.1; -.
DR      HSSP; P35555; 1EMN.
DR      Genew; HGNC:3218; EFEMP1.
DR      MIM; 601548; -.
DR      MIM; 126600; -.
DR      GO; GO:0005578; C:extracellular matrix; TAS.
DR      GO; GO:0007601; P:vision; TAS.
DR      InterPro; IPR000152; Asx_hydroxyl.
DR      InterPro; IPR001881; EGF_Ca.
DR      InterPro; IPR006209; EGF_like.
DR      Pfam; PF00008; EGF; 3.
DR      SMART; SM00179; EGF_CA; 4.
DR      PROSITE; PS00010; ASX_HYDROXYL; 4.
DR      PROSITE; PS00022; EGF_1; FALSE_NEG.
DR      PROSITE; PS01186; EGF_2; 4.
DR      PROSITE; PS01187; EGF_CA; 6.
KW      Repeat; EGF-like domain; Calcium-binding; Glycoprotein; Signal;
KW      Disease mutation; Polymorphism; Alternative splicing.
FT      SIGNAL      1      17      POTENTIAL.
FT      CHAIN      18      493      EGF-CONTAINING FIBULIN-LIKE EXTRACELLULAR
FT                                     MATRIX PROTEIN 1.
FT      DOMAIN      26      71      EGF-LIKE 1, DIVERGENT.
FT      DOMAIN      173     213     EGF-LIKE 2, CALCIUM-BINDING (POTENTIAL).
FT      DOMAIN      214     253     EGF-LIKE 3, CALCIUM-BINDING (POTENTIAL).
FT      DOMAIN      254     293     EGF-LIKE 4, CALCIUM-BINDING (POTENTIAL).
FT      DOMAIN      294     333     EGF-LIKE 5, CALCIUM-BINDING (POTENTIAL).
FT      DOMAIN      334     378     EGF-LIKE 6, CALCIUM-BINDING (POTENTIAL).
FT      DISULFID     177     190     BY SIMILARITY.
FT      DISULFID     184     199     BY SIMILARITY.
FT      DISULFID     201     212     BY SIMILARITY.
FT      DISULFID     218     228     BY SIMILARITY.

```

FT	DISULFID	224	237	BY SIMILARITY.
FT	DISULFID	239	252	BY SIMILARITY.
FT	DISULFID	258	268	BY SIMILARITY.
FT	DISULFID	264	277	BY SIMILARITY.
FT	DISULFID	279	292	BY SIMILARITY.
FT	DISULFID	298	309	BY SIMILARITY.
FT	DISULFID	305	318	BY SIMILARITY.
FT	DISULFID	320	332	BY SIMILARITY.
FT	DISULFID	338	350	BY SIMILARITY.
FT	DISULFID	344	359	BY SIMILARITY.
FT	DISULFID	365	377	BY SIMILARITY.
FT	CARBOHYD	249	249	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	VARSPLIC	1	8	Missing (in isoform 2).
FT				/FTId=VSP_001392.
FT	VARSPLIC	58	58	Missing (in isoform 3).
FT				/FTId=VSP_001393.
FT	VARSPLIC	106	106	Missing (in isoform 4).
FT				/FTId=VSP_001394.
FT	VARIANT	220	220	I -> F.
FT				/FTId=VAR_009512.
FT	VARIANT	345	345	R -> W (IN MVLT).
FT				/FTId=VAR_009513.
SQ	SEQUENCE	493 AA;	54640 MW;	128CA5ED140DF414 CRC64;

Query Match 45.4%; Score 1093.5; DB 1; Length 493;
 Best Local Similarity 43.2%; Pred. No. 3.6e-74;
 Matches 203; Conservative 64; Mismatches 152; Indels 51; Gaps 7;

Qy	1	QCTNGFDLDRQSGQCLDIDECRTIPEACRGDMMCVNQNGGYLCIPRTNPVY---RGPYSN	57
		: : : : : : : :	
Db	28	QCTDGYEWDVPVRQQCKDIDECDIVPDACKGGMKCVNHYGGYLCPLKTAQIIVNNEQPQQE	87
Qy	58	PY-----STPYSGPYPA-----APPL	74
Db	88	TQPAEGTSGATTGVVAASSMATSGVLPGGGFVASAAVAGPEMQTGRNNFVIRRNPPADPQ	147
Qy	75	SAPNYPTISRPLICRFGYQMDENQCVDVDECATDSHCNPTQICINTEGGYTCSCTDGY	134
		: : : : : :	
Db	148	RIPSNP--SHRIQCAAGYEQSEHNVCQDIDECTAGTHNCRADQVCINLRGSFACQCPPGY	205
Qy	135	WLLEGQCLDIDECRY-GYCQQLCANVPGSYSCTCNPGFTLNEDGRSCQDVNECATENPCV	193
		: : :	
Db	206	QKRGEQCVDIDECTIPPYCHQRCVNTPGSFYCQCSPGFQLAANNYTCVDINECDASNQCA	265
Qy	194	QTCVNTYGSFICRCDPGYELEEDGVHCSMDDECSFSEFLCQHECVNQPGTYFCSCPPGYI	253
		: : : : :	
Db	266	QQCYNILGSFICQCNQGYELSSDRLNCEDIDECRTSSYLCQYQCVNEPGKFSMCPQGYQ	325
Qy	254	LLDDNRSCQDINECEHRNHTCNLQQTTCYNLQGGFKCIDPIRCEEPYLRISDNRCMCPAEN	313
		: : : : : : : : : :	
Db	326	VV-RSRTCQDINECETTNE-CREDEMWNHGGFRFCYPRNPCQDPYILTPENRCVCPVSN	383
Qy	314	PGCRDQPFTILYRDMDVVSGRSVPADIFQMQATTRYPGAYYIFQIKSGNEGREFYMRQTG	373
		: : : : :	
Db	384	AMCRELPQSIVYKYMSIRSDRSVPSDIFQIQATTIYANTINTFRIKSGNENGEPYLRQTS	443
Qy	374	PISATLVMTRPIKGPREIQLDLEMITVNTVINFRGSSVIRLRIYVSQYPF	423

Db

444 PVSAMLVLVKSLSGPREHIVDLEMLTVSSIGTFRTSSVLRLTIIVGPFSF 493

RESULT 9

FBL2_MOUSE

ID FBL2_MOUSE STANDARD; PRT; 1221 AA.
AC P37889; Q9WUI2;
DT 01-OCT-1994 (Rel. 30, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Fibulin-2 precursor.
GN FBLN2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A., AND SEQUENCE OF 27-35.
RC TISSUE=Fibroblast;
RX MEDLINE=94064787; PubMed=8245130;
RA Pan T.-C., Sasaki T., Zhang R.-Z., Faessler R., Timpl R., Chu M.-L.;
RT "Structure and expression of fibulin-2, a novel extracellular matrix
RT protein with multiple EGF-like repeats and consensus motifs for
RT calcium binding.";
RL J. Cell Biol. 123:1269-1277(1993).
RN [2]
RP SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.
RX MEDLINE=99337686; PubMed=10406956;
RA Graessel S., Sicot F.-X., Gotta S., Chu M.-L.;
RT "Mouse fibulin-2 gene. Complete exon-intron organization and promoter
RT characterization.";
RL Eur. J. Biochem. 263:471-477(1999).
RN [3]
RP DEVELOPMENTAL STAGE.
RX PubMed=8850569;
RA Zhang H.-Y., Timpl R., Sasaki T., Chu M.-L., Ekblom P.;
RT "Fibulin-1 and fibulin-2 expression during organogenesis in the
RT developing mouse embryo.";
RL Dev. Dyn. 205:348-364(1996).
RN [4]
RP BINDING TO LAMA2.
RX PubMed=10022829;
RA Talts J.F., Andac Z., Goehring W., Brancaccio A., Timpl R.;
RT "Binding of the G domains of laminin alpha1 and alpha2 chains and
RT perlecan to heparin, sulfatides, alpha-dystroglycan and several
RT extracellular matrix proteins.";
RL EMBO J. 18:863-870(1999).
RN [5]
RP DOWN-REGULATION BY GLUCOCORTICOIDS.
RX PubMed=11737251;
RA Gu Y.-C., Talts J.F., Gullberg D., Timpl R., Ekblom M.;
RT "Glucocorticoids down-regulate the extracellular matrix proteins
RT fibronectin, fibulin-1 and fibulin-2 in bone marrow stroma.";
RL Eur. J. Haematol. 67:176-184(2001).
CC -!- FUNCTION: ITS BINDING TO FIBRONECTIN AND SOME OTHER LIGANDS IS
CC CALCIUM DEPENDENT.

```

CC  -!- SUBUNIT: Homotrimer; disulfide-linked. Interacts with LAMA2.
CC  -!- SUBCELLULAR LOCATION: Secreted; extracellular matrix.
CC  -!- ALTERNATIVE PRODUCTS:
CC      Event=Alternative splicing; Named isoforms=2;
CC      Comment=Additional isoforms seem to exist;
CC      Name=1;
CC      IsoId=P37889-1; Sequence=Displayed;
CC      Name=2; Synonyms=EGF3-less;
CC      IsoId=P37889-2; Sequence=VSP_001391;
CC  -!- TISSUE SPECIFICITY: Component of both basement membranes and other
CC      connective tissues.
CC  -!- DEVELOPMENTAL STAGE: The differential expression of the fibulin
CC      family contributes to the formation of molecularly distinct
CC      extracellular matrices already during early developmental stages
CC      of a large number of tissues.
CC  -!- INDUCTION: Glucocorticoids suppressed mRNA expression and protein
CC      synthesis.
CC  -!- SIMILARITY: Belongs to the fibulin family.
CC  -!- SIMILARITY: Contains 3 anaphylatoxin-like domains.
CC  -!- SIMILARITY: Contains 11 EGF-like domains.
CC  -----
CC  This SWISS-PROT entry is copyright. It is produced through a collaboration
CC  between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC  the European Bioinformatics Institute. There are no restrictions on its
CC  use by non-profit institutions as long as its content is in no way
CC  modified and this statement is not removed. Usage by and for commercial
CC  entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC  or send an email to license@isb-sib.ch).
CC  -----
DR  EMBL; X75285; CAA53040.1; -.
DR  EMBL; AF135253; AAD34456.1; -.
DR  EMBL; AF135239; AAD34456.1; JOINED.
DR  EMBL; AF135240; AAD34456.1; JOINED.
DR  EMBL; AF135241; AAD34456.1; JOINED.
DR  EMBL; AF135242; AAD34456.1; JOINED.
DR  EMBL; AF135243; AAD34456.1; JOINED.
DR  EMBL; AF135244; AAD34456.1; JOINED.
DR  EMBL; AF135245; AAD34456.1; JOINED.
DR  EMBL; AF135246; AAD34456.1; JOINED.
DR  EMBL; AF135247; AAD34456.1; JOINED.
DR  EMBL; AF135248; AAD34456.1; JOINED.
DR  EMBL; AF135249; AAD34456.1; JOINED.
DR  EMBL; AF135250; AAD34456.1; JOINED.
DR  EMBL; AF135251; AAD34456.1; JOINED.
DR  EMBL; AF135252; AAD34456.1; JOINED.
DR  PIR; A49457; A49457.
DR  HSSP; P00736; 1APQ.
DR  MGD; MGI:95488; Fbln2.
DR  InterPro; IPR000020; Anaphylatoxin.
DR  InterPro; IPR000152; Asx_hydroxyl.
DR  InterPro; IPR001881; EGF_Ca.
DR  InterPro; IPR006209; EGF_like.
DR  Pfam; PF01821; ANATO; 2.
DR  Pfam; PF00008; EGF; 6.
DR  SMART; SM00104; ANATO; 3.
DR  SMART; SM00179; EGF_CA; 9.
DR  PROSITE; PS00010; ASX_HYDROXYL; 5.

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DR PROSITE; PS01177; ANAPHYLATOXIN_1; 3.
 DR PROSITE; PS01178; ANAPHYLATOXIN_2; 3.
 DR PROSITE; PS00022; EGF_1; FALSE_NEG.
 DR PROSITE; PS01186; EGF_2; 5.
 DR PROSITE; PS01187; EGF_CA; 10.
 KW Signal; Glycoprotein; Extracellular matrix; Plasma; EGF-like domain;
 KW Calcium-binding; Alternative splicing; Repeat.
 FT SIGNAL 1 26
 FT CHAIN 27 1221 FIBULIN-2.
 FT DOMAIN 27 434 N.
 FT DOMAIN 27 176 SUBDOMAIN NA (CYS-RICH).
 FT DOMAIN 177 434 SUBDOMAIN NB (CYS-FREE).
 FT DOMAIN 435 477 ANAPHYLATOXIN-LIKE 1.
 FT DOMAIN 478 510 ANAPHYLATOXIN-LIKE 2.
 FT DOMAIN 511 543 ANAPHYLATOXIN-LIKE 3.
 FT DOMAIN 594 635 EGF-LIKE 1, CALCIUM-BINDING (POTENTIAL).
 FT DOMAIN 669 708 EGF-LIKE 2.
 FT DOMAIN 709 755 EGF-LIKE 3, CALCIUM-BINDING (POTENTIAL).
 FT DOMAIN 756 800 EGF-LIKE 4, CALCIUM-BINDING (POTENTIAL).
 FT DOMAIN 801 846 EGF-LIKE 5, CALCIUM-BINDING (POTENTIAL).
 FT DOMAIN 847 894 EGF-LIKE 6, CALCIUM-BINDING (POTENTIAL).
 FT DOMAIN 895 937 EGF-LIKE 7, CALCIUM-BINDING (POTENTIAL).
 FT DOMAIN 938 979 EGF-LIKE 8, CALCIUM-BINDING (POTENTIAL).
 FT DOMAIN 980 1018 EGF-LIKE 9, CALCIUM-BINDING (POTENTIAL).
 FT DOMAIN 1019 1061 EGF-LIKE 10, CALCIUM-BINDING (POTENTIAL).
 FT DOMAIN 1062 1106 EGF-LIKE 11, CALCIUM-BINDING (POTENTIAL).
 FT DOMAIN 1111 1221 DOMAIN III.
 FT SITE 421 423 CELL ATTACHMENT SITE (POTENTIAL).
 FT DISULFID 435 462 BY SIMILARITY.
 FT DISULFID 436 469 BY SIMILARITY.
 FT DISULFID 449 470 BY SIMILARITY.
 FT DISULFID 479 508 BY SIMILARITY.
 FT DISULFID 492 509 BY SIMILARITY.
 FT DISULFID 511 535 BY SIMILARITY.
 FT DISULFID 512 542 BY SIMILARITY.
 FT DISULFID 525 543 BY SIMILARITY.
 FT DISULFID 598 610 BY SIMILARITY.
 FT DISULFID 606 619 BY SIMILARITY.
 FT DISULFID 621 634 BY SIMILARITY.
 FT DISULFID 673 683 BY SIMILARITY.
 FT DISULFID 679 692 BY SIMILARITY.
 FT DISULFID 694 707 BY SIMILARITY.
 FT DISULFID 713 726 BY SIMILARITY.
 FT DISULFID 720 735 BY SIMILARITY.
 FT DISULFID 742 754 BY SIMILARITY.
 FT DISULFID 805 818 BY SIMILARITY.
 FT DISULFID 812 827 BY SIMILARITY.
 FT DISULFID 833 845 BY SIMILARITY.
 FT DISULFID 899 912 BY SIMILARITY.
 FT DISULFID 906 921 BY SIMILARITY.
 FT DISULFID 923 936 BY SIMILARITY.
 FT DISULFID 942 954 BY SIMILARITY.
 FT DISULFID 950 963 BY SIMILARITY.
 FT DISULFID 965 978 BY SIMILARITY.
 FT DISULFID 984 993 BY SIMILARITY.
 FT DISULFID 989 1002 BY SIMILARITY.
 FT DISULFID 1004 1017 BY SIMILARITY.

FT	DISULFID	1023	1035	BY SIMILARITY.
FT	DISULFID	1031	1044	BY SIMILARITY.
FT	DISULFID	1046	1060	BY SIMILARITY.
FT	DISULFID	1066	1079	BY SIMILARITY.
FT	DISULFID	1073	1088	BY SIMILARITY.
FT	DISULFID	1093	1105	BY SIMILARITY.
FT	CARBOHYD	179	179	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	497	497	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	737	737	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	1072	1072	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	VARSPLIC	709	755	Missing (in isoform 2).
FT				/FTid=VSP_001391.
FT	CONFLICT	140	159	HSGRKYAAGHTVHLSSCRAC -> TVAVSICWPYRPLILP
FT				GF (IN REF. 2).
FT	CONFLICT	348	348	S -> L (IN REF. 2).
FT	CONFLICT	507	507	Q -> QQ (IN REF. 2).
FT	CONFLICT	1102	1102	Q -> E (IN REF. 2).
SQ	SEQUENCE	1221 AA;	131818 MW;	87DB2A10A8FDC45F CRC64;

Query Match 30.3%; Score 729.5; DB 1; Length 1221;
 Best Local Similarity 35.3%; Pred. No. 9e-47;
 Matches 145; Conservative 59; Mismatches 148; Indels 59; Gaps 11;

Qy	1	QCTNGFDLDRQSGQCLDIDECRTIPEACRGDMMCVNQNGGYLCIPRTNPVYRGPYSPNPYS	60
		: : : : : : :	
Db	832	RCMDGF-LQDPEGNCVDINECTSLLEPCRS GFSCINTVGSYTC-----	873
Qy	61	TPYSGPYPAAPPLSAPNYPTISRPLICRFGYQM-DESNQCVDVDECATDSHCNPTQIC	119
		: : : : : :	
Db	874	-----QRNPLVCGRGYHANEESGSECVDVNECETGVHRCGEGQLC	912
Qy	120	INTEGGYTCSDTDGYW--LLEGQCLDIDECRYG---YCQQLCANVPGSYSCTCNPGFTLN	174
		: : : :	
Db	913	YNLPGSYRCDCKPGFQRDAFGRTCIDVNECWVSPGRLCQHTCENTPGSYRSCAAGFLLA	972
Qy	175	EDGRSCQDVNECATENPCVQTCVNTYGSFICRCDPGYELEEDGVHCSMDDECS-FSEFLC	233
		: : : : : : :	
Db	973	ADGKHCEDVNECETRR-CSQECANIYGSYQCYCRQGYQLAEDGHTCTDIDECAQGAGILC	1031
Qy	234	QHECVNQPGTYFCSCP-PGYILLDDNRSCQDINECEHRNHTCNLQQTCTYNLQGGFKCIDP	292
		: : : : : : : : : :	
Db	1032	TFRCVNVPGSYQCACPEQGYTMMANGRSCKDLDECALGTHNCSEAETCHNIQGSFRCL-R	1090
Qy	293	IRCEEPYLRISDNRCMCPAENPGCRD-----QPFTILYRDMDVVSGRSVPADIFQMQAT	346
		: : : : : : : :	
Db	1091	FDCPPNYVRVSQTKC----ERTTCQDITECQTSPARITHYQLNFQTGLLVPAHIFRIGPA	1146
Qy	347	TRYPGAYYIFQIKSGNEGREFYMRQTGPISATLVMTRPIKGPREIQLDLEM	397
		: : : : : : :	
Db	1147	PAFAGDTISLTITKGNEEGYFVTRRLNAYTGVSLSQSVLEPRDFALDVEM	1197

RESULT 10
 FBL1_CERAE
 ID FBL1_CERAE STANDARD; PRT; 598 AA.
 AC Q8MJJ9;
 DT 15-SEP-2003 (Rel. 42, Created)

DT 15-SEP-2003 (Rel. 42, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Fibulin-1C (Fragment).
 GN FBLN1.
 OS Cercopithecus aethiops (Green monkey) (Grivet).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
 OC Cercopithecinae; Cercopithecus.
 OX NCBI_TaxID=9534;
 RN [1]
 RP SEQUENCE FROM N.A., AND INTERACTION WITH DTR.
 RX PubMed=11846885;
 RA Brooke J.S., Cha J.-H., Eidels L.;
 RT "Latent transforming growth factor beta-binding protein-3 and
 RT fibulin-1C interact with the extracellular domain of the
 RT heparin-binding EGF-like growth factor precursor.";
 RL BMC Cell Biol. 3:2-2(2002).
 CC -!- FUNCTION: Incorporated into fibronectin-containing matrix fibers.
 CC May play a role in cell adhesion and migration along protein
 CC fibers within the extracellular matrix (ECM). Could be important
 CC for certain developmental processes and contribute to the
 CC supramolecular organization of ECM architecture, in particular to
 CC those of basement membranes. May serve to anchor the
 CC mature/soluble form of DTR to its fibers as it migrates through
 CC the extracellular matrix. The direct physical association with DTR
 CC may be useful in such tissue developmental processes as wound
 CC healing.
 CC -!- SUBUNIT: Interacts with itself and with various extracellular
 CC matrix components (By similarity). Interacts with the
 CC mature/soluble form of DTR.
 CC -!- SUBCELLULAR LOCATION: Secreted; extracellular matrix.
 CC -!- SIMILARITY: Belongs to the fibulin family.
 CC -!- SIMILARITY: Contains at least 2 anaphylatoxin-like domains.
 CC -!- SIMILARITY: Contains 9 EGF-like domains.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; AF395659; AAM90567.1; -.
 DR InterPro; IPR000020; Anaphylatoxin.
 DR InterPro; IPR000152; Asx_hydroxyl.
 DR InterPro; IPR001881; EGF_Ca.
 DR InterPro; IPR006209; EGF_like.
 DR InterPro; IPR006210; IEGF.
 DR Pfam; PF01821; ANATO; 1.
 DR Pfam; PF00008; EGF; 5.
 DR SMART; SM00104; ANATO; 1.
 DR SMART; SM00181; EGF; 9.
 DR SMART; SM00179; EGF_CA; 9.
 DR PROSITE; PS01177; ANAPHYLATOXIN_1; 1.
 DR PROSITE; PS01178; ANAPHYLATOXIN_2; 1.
 DR PROSITE; PS00010; ASX_HYDROXYL; 4.

DR PROSITE; PS01186; EGF_2; 3.
DR PROSITE; PS01187; EGF_CA; 7.
KW Glycoprotein; Extracellular matrix; Repeat; EGF-like domain;
KW Calcium-binding.

FT	NON_TER	1	1	
FT	CHAIN	<1	598	FIBULIN-1C.
FT	DOMAIN	<1	27	ANAPHYLATOXIN-LIKE 2.
FT	DOMAIN	28	60	ANAPHYLATOXIN-LIKE 3.
FT	DOMAIN	92	131	EGF-LIKE 1.
FT	DOMAIN	132	177	EGF-LIKE 2, CALCIUM-BINDING (POTENTIAL).
FT	DOMAIN	178	223	EGF-LIKE 3, CALCIUM-BINDING (POTENTIAL).
FT	DOMAIN	224	270	EGF-LIKE 4, CALCIUM-BINDING (POTENTIAL).
FT	DOMAIN	271	313	EGF-LIKE 5, CALCIUM-BINDING (POTENTIAL).
FT	DOMAIN	314	355	EGF-LIKE 6, CALCIUM-BINDING (POTENTIAL).
FT	DOMAIN	356	395	EGF-LIKE 7, CALCIUM-BINDING (POTENTIAL).
FT	DOMAIN	396	439	EGF-LIKE 8, CALCIUM-BINDING (POTENTIAL).
FT	DOMAIN	440	484	EGF-LIKE 9, CALCIUM-BINDING (POTENTIAL).
FT	DOMAIN	271	355	SELF-ASSOCIATION AND FN1-BINDING (BY
FT				SIMILARITY).
FT	DISULFID	<1	25	BY SIMILARITY.
FT	DISULFID	7	26	BY SIMILARITY.
FT	DISULFID	28	52	BY SIMILARITY.
FT	DISULFID	29	59	BY SIMILARITY.
FT	DISULFID	42	60	BY SIMILARITY.
FT	DISULFID	96	106	BY SIMILARITY.
FT	DISULFID	102	115	BY SIMILARITY.
FT	DISULFID	117	130	BY SIMILARITY.
FT	DISULFID	136	149	BY SIMILARITY.
FT	DISULFID	143	158	BY SIMILARITY.
FT	DISULFID	164	176	BY SIMILARITY.
FT	DISULFID	182	195	BY SIMILARITY.
FT	DISULFID	189	204	BY SIMILARITY.
FT	DISULFID	210	222	BY SIMILARITY.
FT	DISULFID	228	242	BY SIMILARITY.
FT	DISULFID	257	270	BY SIMILARITY.
FT	DISULFID	275	288	BY SIMILARITY.
FT	DISULFID	282	297	BY SIMILARITY.
FT	DISULFID	299	312	BY SIMILARITY.
FT	DISULFID	318	330	BY SIMILARITY.
FT	DISULFID	326	339	BY SIMILARITY.
FT	DISULFID	341	354	BY SIMILARITY.
FT	DISULFID	360	369	BY SIMILARITY.
FT	DISULFID	365	378	BY SIMILARITY.
FT	DISULFID	380	394	BY SIMILARITY.
FT	DISULFID	400	413	BY SIMILARITY.
FT	DISULFID	409	422	BY SIMILARITY.
FT	DISULFID	424	438	BY SIMILARITY.
FT	DISULFID	444	457	BY SIMILARITY.
FT	DISULFID	451	466	BY SIMILARITY.
FT	DISULFID	471	483	BY SIMILARITY.
FT	CARBOHYD	14	14	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	450	450	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	454	454	N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ	SEQUENCE	598 AA;	65516 MW;	849BF018DF452B02 CRC64;

Query Match 30.0%; Score 721; DB 1; Length 598;
Best Local Similarity 35.3%; Pred. No. 1.9e-46;

Matches 155; Conservative 72; Mismatches 184; Indels 28; Gaps 15;

```
Qy      2 CTNGFDLDRQSGQCLDIDECRTIPEACRGDMMCVNQNGGYLCIPR---TNPVYRGPYSNP 58
      | |::| : | |||:| : | | :| | : | | : | : |
Db     164 CGTGYEL-TEDNSCKDIDQCESGIHNCLPDFICQNTLGSFRCRPKLQCKNGFIQDALANC 222

Qy     59 YS-----TPYSGPYPAAPPLSAPNYPTISRPLICRFGYQMDESNQCVDVDECATDSHC 113
      : | | | : : | | | : : | | : : | | : |
Db     223 IDINECLSIVSAPCPTGHTCINTEGSYTQKNVPNCGRGYHLNEEGTRCDVNECAPPAEPC 282

Qy    114 NPTQICINTEGGYTCSCTDGYWL--LEGQCLDIDEC-RY--GYCQQLCANVPGSYSCTCN 168
      |::| : | | ||: : |::|| | | | | | | | | | | |
Db    283 GKGHRCVNSPGSFRCECKTGYIFYDGI SRMCVDVNECQRYPGRLCGHKCENTLGSYVCS 342

Qy    169 PGFTLNEDGRSCQDVNECATENPCVQTCVNTYGSFICRCDPGYELEE-DGVHCSDMDECS 227
      || | : |||||:|:|:|:|:|:| | | | | | | | | | | |
Db    343 VGFRLSVDGRSCEDINECSS-SPCSQECANVYGSYQCYCRRGYQLSDVDGVTCEDIDEC 401

Qy    228 F--SEFLCQHECVNQPGTYFCSCP-PGYILLDDNRSCQDINECEHRNHTCNLQQTTCYNLQ 284
      : | : | : | ||:| || | | | : | : ||||:| | | | : | : | : |
Db    402 LPTGGHICSYRCINIPGSFQCSCPASGYRLAPNGRNCQDIDECVTGIHNCSINETCFNIQ 461

Qy    285 GGFKCIDPIRCEEPYLRISDNRC-MCPA-ENPGCRDQPFTILYRDMDVVSGRSVPADIFQ 342
      |||:|: | | | | : | | | | | | | | : : | | : |
Db    462 GGFRCL-AFECPENYRRSAATRCERLPCHENRECSKPLRITYYHLSFPTNIQAPAVVFR 520

Qy    343 MQATTRYPGAYYIFQIKSGNEGREFYMRQTGPISATLVMTRPIKGPREIQLDLEM--ITV 400
      | : : | | | | | | | | : | | : : | : | | : : |
Db    521 MGPSSAVPGDSMQLAITGGNEEGFFTTRKVSPHSGVVALTKPVPEPRDLLLTVMKMDLYRH 580

Qy    401 NTVINFRGSSVIRLRIYVS 419
      || : | | : | | : ||
Db    581 GTVSSF----VAKLFIFVS 595
```

RESULT 11

FBL1_CHICK

ID FBL1_CHICK STANDARD; PRT; 704 AA.
AC O73775; O73774;
DT 16-OCT-2001 (Rel. 40, Created)
DT 15-SEP-2003 (Rel. 42, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Fibulin-1 precursor.
GN FBLN1.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORMS C AND D).
RC TISSUE=Embryo;
RX MEDLINE=99120531; PubMed=9923656;
RA Barth J.L., Argraves K.M., Roark E.F., Little C.D., Argraves W.S.;
RT "Identification of chicken and C. elegans fibulin-1 homologs and
RT characterization of the C. elegans fibulin-1 gene.";
RL Matrix Biol. 17:635-646(1998).

```

CC  -!- FUNCTION: Incorporated into fibronectin-containing matrix fibers.
CC      May play a role in cell adhesion and migration along protein
CC      fibers within the extracellular matrix (ECM). Could be important
CC      for certain developmental processes and contribute to the
CC      supramolecular organization of ECM architecture, in particular to
CC      those of basement membranes.
CC  -!- SUBUNIT: Interacts with itself and with various extracellular
CC      matrix components (By similarity).
CC  -!- SUBCELLULAR LOCATION: Secreted; extracellular matrix.
CC  -!- ALTERNATIVE PRODUCTS:
CC      Event=Alternative splicing; Named isoforms=2;
CC      Name=D;
CC          IsoId=O73775-2; Sequence=Displayed;
CC      Name=C;
CC          IsoId=O73775-1; Sequence=VSP_007378;
CC  -!- SIMILARITY: Belongs to the fibulin family.
CC  -!- SIMILARITY: Contains 3 anaphylatoxin-like domains.
CC  -!- SIMILARITY: Contains 9 EGF-like domains.
CC  -----
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CC  the European Bioinformatics Institute. There are no restrictions on its
CC  use by non-profit institutions as long as its content is in no way
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CC  entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC  or send an email to license@isb-sib.ch).
CC  -----
DR  EMBL; AF051399; AAC05387.1; -.
DR  EMBL; AF051400; AAC05388.1; -.
DR  HSSP; P00742; 1HCG.
DR  InterPro; IPR000020; Anaphylatoxin.
DR  InterPro; IPR000152; Asx_hydroxyl.
DR  InterPro; IPR001881; EGF_Ca.
DR  InterPro; IPR006209; EGF_like.
DR  Pfam; PF01821; ANATO; 2.
DR  Pfam; PF00008; EGF; 6.
DR  SMART; SM00104; ANATO; 3.
DR  SMART; SM00181; EGF; 9.
DR  SMART; SM00179; EGF_CA; 8.
DR  PROSITE; PS00010; ASX_HYDROXYL; 5.
DR  PROSITE; PS01177; ANAPHYLATOXIN_1; 1.
DR  PROSITE; PS01178; ANAPHYLATOXIN_2; 2.
DR  PROSITE; PS00022; EGF_1; FALSE_NEG.
DR  PROSITE; PS01186; EGF_2; 3.
DR  PROSITE; PS01187; EGF_CA; 8.
KW  Signal; Alternative splicing; Glycoprotein; Extracellular matrix;
KW  Repeat; EGF-like domain; Calcium-binding.
FT  SIGNAL          1      25      POTENTIAL.
FT  CHAIN           26     704      FIBULIN-1.
FT  DOMAIN          33      74      ANAPHYLATOXIN-LIKE 1.
FT  DOMAIN          75     109      ANAPHYLATOXIN-LIKE 2.
FT  DOMAIN         110     142      ANAPHYLATOXIN-LIKE 3.
FT  DOMAIN          177     216      EGF-LIKE 1.
FT  DOMAIN          217     262      EGF-LIKE 2, CALCIUM-BINDING (POTENTIAL).
FT  DOMAIN          263     308      EGF-LIKE 3, CALCIUM-BINDING (POTENTIAL).
FT  DOMAIN          309     356      EGF-LIKE 4, CALCIUM-BINDING (POTENTIAL).
FT  DOMAIN          357     399      EGF-LIKE 5, CALCIUM-BINDING (POTENTIAL).

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FT	DOMAIN	400	441	EGF-LIKE 6, CALCIUM-BINDING (POTENTIAL).
FT	DOMAIN	442	481	EGF-LIKE 7, CALCIUM-BINDING (POTENTIAL).
FT	DOMAIN	482	525	EGF-LIKE 8, CALCIUM-BINDING (POTENTIAL).
FT	DOMAIN	526	579	EGF-LIKE 9, CALCIUM-BINDING (POTENTIAL).
FT	DOMAIN	357	441	SELF-ASSOCIATION AND FN1-BINDING (BY
FT				SIMILARITY).
FT	DISULFID	33	59	BY SIMILARITY.
FT	DISULFID	34	66	BY SIMILARITY.
FT	DISULFID	47	67	BY SIMILARITY.
FT	DISULFID	76	107	BY SIMILARITY.
FT	DISULFID	89	108	BY SIMILARITY.
FT	DISULFID	110	134	BY SIMILARITY.
FT	DISULFID	111	141	BY SIMILARITY.
FT	DISULFID	124	142	BY SIMILARITY.
FT	DISULFID	181	191	BY SIMILARITY.
FT	DISULFID	187	200	BY SIMILARITY.
FT	DISULFID	202	215	BY SIMILARITY.
FT	DISULFID	221	234	BY SIMILARITY.
FT	DISULFID	228	243	BY SIMILARITY.
FT	DISULFID	249	261	BY SIMILARITY.
FT	DISULFID	267	280	BY SIMILARITY.
FT	DISULFID	274	289	BY SIMILARITY.
FT	DISULFID	295	307	BY SIMILARITY.
FT	DISULFID	313	326	BY SIMILARITY.
FT	DISULFID	320	335	BY SIMILARITY.
FT	DISULFID	342	355	BY SIMILARITY.
FT	DISULFID	361	374	BY SIMILARITY.
FT	DISULFID	368	383	BY SIMILARITY.
FT	DISULFID	385	398	BY SIMILARITY.
FT	DISULFID	404	416	BY SIMILARITY.
FT	DISULFID	412	425	BY SIMILARITY.
FT	DISULFID	427	440	BY SIMILARITY.
FT	DISULFID	446	455	BY SIMILARITY.
FT	DISULFID	451	464	BY SIMILARITY.
FT	DISULFID	466	480	BY SIMILARITY.
FT	DISULFID	486	499	BY SIMILARITY.
FT	DISULFID	495	508	BY SIMILARITY.
FT	DISULFID	510	524	BY SIMILARITY.
FT	DISULFID	530	543	BY SIMILARITY.
FT	DISULFID	537	552	BY SIMILARITY.
FT	DISULFID	557	578	BY SIMILARITY.
FT	CARBOHYD	96	96	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	536	536	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	540	540	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	VARSPLIC	568	704	VRLEKTDITIRCIKSCRPNVDVNCVLDPVHTISHTVISLPTFR
FT				EFTRPEEIIIFLRAITPTYPANQADIIIFDITEGNLRESFDII
FT				KRYMDGMTVGVVRQVRPIVGPFHAILKLEMNYVMGGVVSHR
FT				NIVNVHIFVSEYWF -> RCERLPCNENKECQSLPLRITYY
FT				HLSFPTNIQVPTDIFRMGPSNAVPGDKILLSIISGNQEGFF
FT				TTKKVNNHSGIVVMQRQITEPRDLLLTIQMLTRHGTVNTF
FT				IAKLFVVFVSAQL (in isoform C).
FT				/FTId=VSP_007378.
SQ	SEQUENCE	704 AA;	78137 MW;	D47D5A30D5E42932 CRC64;

Query Match 29.6%; Score 713; DB 1; Length 704;
 Best Local Similarity 35.1%; Pred. No. 8.8e-46;
 Matches 160; Conservative 64; Mismatches 154; Indels 78; Gaps 21;

Qy 1 QCTNGFDLDRQSGQCLDIDECRTIPEACRGDMMCVNQNGGYLCIPRTNPVYRGPYSNPYS 60
 || ||| | | :||:| | : | :|:| | | | :|
 Db 294 QCMNGFIQD-ALGNCIDINECLSTNMPCPAGQICINTDGSYTC-QRISP----- 340

Qy 61 TPYSGPYPAAPPLSAPNYPTISRPLICRFGYQMDE-SNQCVDVDECATDSHCNPTQIC 119
 | || :| :||| ||| :| :|
 Db 341 -----SCGRGYHLNEDGTRCVDVDECSSDQPCGEGHVC 374

Qy 120 INTEGgyTCsCTDgyw--LLEGQCLDIDECRY---GYCQQLCANVPGSYsCTCNPGFTLN 174
 || | | | | || :| :||:| | | | | | | | | | | :|
 Db 375 INGPGNYRCECKSGYSFDVISRTCIDINECRRYPGRLCAHKCENTPGSYyCTCTMGFKLS 434

Qy 175 EDGRSCQDVNECATENPCVQTCVNTYGSFICRCDPGYELEE-DGVHCSDMDECSF--SEF 231
 |||||:|:| | : || | | | |||: | | :|:| : | :| | :| | :|
 Db 435 SDGRSCEDLNECES-SPCSQECANVYGSYQCYCRRGFQLSDIDGISCEDIDECALPTGGH 493

Qy 232 LCQHECVNQPGTYFCSCP-PGYILLDDNRSCQDINECEHRNHTCNLQQTCYNLQGGFKCI 290
 :| | :| ||:| :|| | | | : | :|||:| | | | :| :| :| :| :| :| :|
 Db 494 ICSFRCINIPGSFQCTCPSTGYRLAPNARNCQDIDECVAETHNCSFNCTCFNIQGGFRCL 553

Qy 291 DPIRCEEPYLRISDN-----RCM--CPAENPGC-RDQPFTILYRDMDVVSGRSV-- 336
 : | | | : | ||: | : | | | : : : |
 Db 554 S-LECPENYRKSGDTRVLEKTDITIRCIKSCRPNVDNVCVLDPVHTISHTVISLPTFREFT 612

Qy 337 PADIFQMQA-TTRYPG--AYYIFQIKSGNEGREF-----YMRQTGPISATLVMTRPIKGP 388
 | :| :| | | | | | | | | | | | : | | | |
 Db 613 PEEIIFLRAITPTYPANQADIIFDITEGNLRESFDIIKRYM--DGMTVGVVVRQVRPIVGP 670

Qy 389 REIQLDLEM-ITVNTVINFRGSSVIRLRIYVSQYPF 423
 | ||| : | :| :| :| :| :| :| :|
 Db 671 FHAILKLEMNYVMGGVVSHR--NIVNVHIFVSEYWF 704

RESULT 12

FBL2_HUMAN

ID FBL2_HUMAN STANDARD; PRT; 1184 AA.
 AC P98095;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Fibulin-2 precursor.
 GN FBLN2.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Fibroblast;
 RX MEDLINE=95104855; PubMed=7806230;
 RA Zhang R.-Z., Pan T.-C., Zhang Z.-Y., Mattei M.-G., Timpl R.,
 RA Chu M.-L.;
 RT "Fibulin-2 (FBLN2): human cDNA sequence, mRNA expression, and mapping
 RT of the gene on human and mouse chromosomes.";
 RL Genomics 22:425-430(1994).
 RN [2]

RP DEVELOPMENTAL STAGE.
RX PubMed=8737292;
RA Miosge N., Gotz W., Sasaki T., Chu M.-L., Timpl R., Herken R.;
RT "The extracellular matrix proteins fibulin-1 and fibulin-2 in the
RT early human embryo.";
RL Histochem. J. 28:109-116(1996).
CC -!- FUNCTION: ITS BINDING TO FIBRONECTIN AND SOME OTHER LIGANDS IS
CC CALCIUM DEPENDENT.
CC -!- SUBUNIT: Homotrimer; disulfide-linked. Interacts with LAMA2 (By
CC similarity).
CC -!- SUBCELLULAR LOCATION: Secreted; extracellular matrix.
CC -!- TISSUE SPECIFICITY: Component of both basement membranes and other
CC connective tissues. Expressed in heart, placenta and ovary.
CC -!- DEVELOPMENTAL STAGE: Widely expressed during embryonic
CC development. Primarily detected within the neuropithelium, spinal
CC ganglia and peripheral nerves.
CC -!- SIMILARITY: Belongs to the fibulin family.
CC -!- SIMILARITY: Contains 3 anaphylatoxin-like domains.
CC -!- SIMILARITY: Contains 11 EGF-like domains.
CC -----
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CC -----
DR EMBL; X82494; CAA57876.1; -.
DR PIR; A55184; A55184.
DR HSSP; P00736; 1APQ.
DR Genew; HGNC:3601; FBLN2.
DR MIM; 135821; -.
DR GO; GO:0005578; C:extracellular matrix; TAS.
DR GO; GO:0005509; F:calcium ion binding activity; TAS.
DR GO; GO:0005207; F:extracellular matrix glycoprotein; TAS.
DR InterPro; IPR000020; Anaphylatoxin.
DR InterPro; IPR000152; Asx_hydroxyl.
DR InterPro; IPR001881; EGF_Ca.
DR InterPro; IPR006209; EGF_like.
DR Pfam; PF01821; ANATO; 2.
DR Pfam; PF00008; EGF; 7.
DR SMART; SM00104; ANATO; 3.
DR SMART; SM00179; EGF_CA; 9.
DR PROSITE; PS00010; ASX_HYDROXYL; 5.
DR PROSITE; PS01177; ANAPHYLATOXIN_1; 3.
DR PROSITE; PS01178; ANAPHYLATOXIN_2; 3.
DR PROSITE; PS00022; EGF_1; FALSE_NEG.
DR PROSITE; PS01186; EGF_2; 5.
DR PROSITE; PS01187; EGF_CA; 9.
KW Signal; Glycoprotein; Extracellular matrix; Plasma; EGF-like domain;
KW Calcium-binding; Repeat.
FT SIGNAL 1 27 POTENTIAL.
FT CHAIN 28 1184 FIBULIN-2.
FT DOMAIN 28 444 N.
FT DOMAIN 28 177 SUBDOMAIN NA (CYS-RICH).
FT DOMAIN 178 444 SUBDOMAIN NB (CYS-FREE).

FT	DOMAIN	445	480	ANAPHYLATOXIN-LIKE 1.
FT	DOMAIN	488	519	ANAPHYLATOXIN-LIKE 2.
FT	DOMAIN	521	553	ANAPHYLATOXIN-LIKE 3.
FT	DOMAIN	604	645	EGF-LIKE 1, CALCIUM-BINDING.
FT	DOMAIN	679	718	EGF-LIKE 2.
FT	DOMAIN	719	763	EGF-LIKE 3, CALCIUM-BINDING.
FT	DOMAIN	764	809	EGF-LIKE 4, CALCIUM-BINDING.
FT	DOMAIN	810	857	EGF-LIKE 5, CALCIUM-BINDING.
FT	DOMAIN	858	900	EGF-LIKE 6, CALCIUM-BINDING.
FT	DOMAIN	901	942	EGF-LIKE 7, CALCIUM-BINDING.
FT	DOMAIN	943	981	EGF-LIKE 8, CALCIUM-BINDING.
FT	DOMAIN	982	1024	EGF-LIKE 9, CALCIUM-BINDING.
FT	DOMAIN	1025	1069	EGF-LIKE 10, CALCIUM-BINDING.
FT	DOMAIN	1070	1184	DOMAIN III.
FT	DISULFID	445	472	BY SIMILARITY.
FT	DISULFID	446	479	BY SIMILARITY.
FT	DISULFID	459	480	BY SIMILARITY.
FT	DISULFID	489	518	BY SIMILARITY.
FT	DISULFID	502	519	BY SIMILARITY.
FT	DISULFID	521	545	BY SIMILARITY.
FT	DISULFID	522	552	BY SIMILARITY.
FT	DISULFID	535	553	BY SIMILARITY.
FT	DISULFID	608	620	BY SIMILARITY.
FT	DISULFID	616	629	BY SIMILARITY.
FT	DISULFID	631	644	BY SIMILARITY.
FT	DISULFID	683	693	BY SIMILARITY.
FT	DISULFID	689	702	BY SIMILARITY.
FT	DISULFID	704	717	BY SIMILARITY.
FT	DISULFID	723	736	BY SIMILARITY.
FT	DISULFID	730	745	BY SIMILARITY.
FT	DISULFID	751	762	BY SIMILARITY.
FT	DISULFID	768	781	BY SIMILARITY.
FT	DISULFID	775	790	BY SIMILARITY.
FT	DISULFID	796	808	BY SIMILARITY.
FT	DISULFID	814	827	BY SIMILARITY.
FT	DISULFID	821	836	BY SIMILARITY.
FT	DISULFID	843	856	BY SIMILARITY.
FT	DISULFID	862	875	BY SIMILARITY.
FT	DISULFID	869	884	BY SIMILARITY.
FT	DISULFID	886	899	BY SIMILARITY.
FT	DISULFID	905	917	BY SIMILARITY.
FT	DISULFID	913	926	BY SIMILARITY.
FT	DISULFID	928	941	BY SIMILARITY.
FT	DISULFID	947	956	BY SIMILARITY.
FT	DISULFID	952	965	BY SIMILARITY.
FT	DISULFID	967	980	BY SIMILARITY.
FT	DISULFID	986	998	BY SIMILARITY.
FT	DISULFID	994	1007	BY SIMILARITY.
FT	DISULFID	1009	1023	BY SIMILARITY.
FT	DISULFID	1029	1042	BY SIMILARITY.
FT	DISULFID	1036	1051	BY SIMILARITY.
FT	DISULFID	1056	1068	BY SIMILARITY.
FT	CARBOHYD	180	180	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	507	507	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	1035	1035	N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ	SEQUENCE	1184	AA; 126543 MW; CA48490A55F9EC5D CRC64;	

Query Match 29.1%; Score 701.5; DB 1; Length 1184;
 Best Local Similarity 34.5%; Pred. No. 1e-44;
 Matches 142; Conservative 58; Mismatches 152; Indels 59; Gaps 11;

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Qy      1 QCTNGFDLDRQSGQCLDIDECRTIPEACRGDMMCVNQNGGYLCIPRTNPVYRGPYSNPYS 60
      :| :|| | | :|:|:| | :| | | | :| | | |
Db      795 RCMDGF-LQDPEGNCVDINECTSLSEPCRPFGFSCINTVGSYTC----- 836

Qy      61 TPYSGPYPAAPPLSAPNYPTISRPLICRFGYQ-MDESNQCVDVDECATDSHCNPTQIC 119
      |||| | | :| :|||:| | | :| | :|
Db      837 -----QRNPLICARGYHASDDGAKCVDVNECETGVHRCGEGQVC 875

Qy     120 INTEGgyTCSTdgyw--LLEGQCLDIDECRYG--YCQQLCANVPGSYSCTCNPGFTLN 174
      | | | | | :| :|:|:| | | | | | | | | |
Db     876 HNLPGSYRCDCkAGfQrDAfGRGCI DVNECWASPGRLCQHTCENTLGsyrcscasgflLA 935

Qy     175 EDGRSCQDVNECATENPCVQTCVNTYGSFICRCDPGYELEEDGVHCSDMDECS-FSEFLC 233
      ||: |:|||| | :| | | | ||: | | ||: ||| |:|:| |: : ||
Db     936 ADGKRCEdVNECEaQR-CSQECANIYGSYQCYCRQGYQLAEDGHTCTDIDeCAQGAGILC 994

Qy     234 QHECVNQPGTYFCSCP-PGYILLDDNRSCQDINECEHRNHTCNLQQTcyNLQGGFKCIDP 292
      |:| ||:| |:| | | : : |||:|:| | | :| :||:|:| |:|:
Db     995 TFRCLNVPGSYQCACPEQGYTMTANGRSCKDVDECALGTHNCSEAETCHNIQGSFRCL-R 1053

Qy     293 IRCEEPYLRISDNRCMCPAENPGCRD-----QPFTILYRDMDVVSGRSVPADIFQMqAT 346
      | | :|:| :| | | | | | | :| :| :| | | | :|
Db    1054 FECPPNYVQVSKTKC----ERTTCHDFLEcQNSPARITHYQLNFQTGLLVPAHIFRIGPA 1109

Qy     347 TRYPGAYYIFQIKSGNEGREFYMRQTGPISATLVMTRPIKGPREIQLDLEM 397
      :| | | | | | :| :|:| | :| | | :|:|
Db    1110 PAFTGDTIALNIiKGNEEGYfGTRRLNAYtGVVYLQRAVLEPRDFALDVEM 1160
  
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RESULT 13

FBL1_HUMAN

ID FBL1_HUMAN STANDARD; PRT; 703 AA.
 AC P23142; P23143; P23144; P37888; Q8TBH8; Q9HBQ5; Q9UGR4; Q9UH41;
 DT 01-NOV-1991 (Rel. 20, Created)
 DT 15-SEP-2003 (Rel. 42, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Fibulin-1 precursor.
 GN FBLN1.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A. (ISOFORMS A; B AND C).
 RX MEDLINE=91100426; PubMed=2269669;
 RA Argaves W.S., Tran H., Burgess W.H., Dickerson K.;
 RT "Fibulin is an extracellular matrix and plasma glycoprotein with
 RT repeated domain structure.";
 RL J. Cell Biol. 111:3155-3164(1990).
 RN [2]
 RP SEQUENCE FROM N.A. (ISOFORM D), TISSUE SPECIFICITY, AND INTERACTION
 RP WITH FN1 AND FGB.
 RX PubMed=9106159;

RA Tran H., Mattei M., Godyna S., Argraves W.S.;
 RT "Human fibulin-1D: molecular cloning, expression and similarity with
 RT S1-5 protein, a new member of the fibulin gene family.";
 RL Matrix Biol. 15:479-493(1997).
 RN [3]
 RP SEQUENCE FROM N.A. (ISOFORM D).
 RX MEDLINE=99253993; PubMed=10318851;
 RA Krichevsky A.M., Metzger E., Rosen H.;
 RT "Translational control of specific genes during differentiation of
 RT HL-60 cells.";
 RL J. Biol. Chem. 274:14295-14305(1999).
 RN [4]
 RP SEQUENCE FROM N.A. (ISOFORM C).
 RA Gu J.R., Wan D.F., Zhao X.T., Zhou X.M., Jiang H.Q., Zhang P.P.,
 RA Qin W.X., Huang Y., Qiu X.K., Qian L.F., He L.P., Li H.N., Yu Y.,
 RA Yu J., Han L.H.;
 RT "Novel Human cDNA clones with function of inhibiting cancer cell
 RT growth.";
 RL Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases.
 RN [5]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20057165; PubMed=10591208;
 RA Dunham I., Hunt A.R., Collins J.E., Bruskiewich R., Beare D.M.,
 RA Clamp M., Smink L.J., Ainscough R., Almeida J.P., Babbage A.K.,
 RA Bagguley C., Bailey J., Barlow K.F., Bates K.N., Beasley O.P.,
 RA Bird C.P., Blakey S.E., Bridgeman A.M., Buck D., Burgess J.,
 RA Burrill W.D., Burton J., Carder C., Carter N.P., Chen Y., Clark G.,
 RA Clegg S.M., Copley V.E., Cole C.G., Collier R.E., Connor R.,
 RA Conroy D., Corby N.R., Coville G.J., Cox A.V., Davis J., Dawson E.,
 RA Dhami P.D., Dockree C., Dodsworth S.J., Durbin R.M., Ellington A.G.,
 RA Evans K.L., Fey J.M., Fleming K., French L., Garner A.A.,
 RA Gilbert J.G.R., Goward M.E., Grafham D.V., Griffiths M.N.D., Hall C.,
 RA Hall R.E., Hall-Tamlyn G., Heathcote R.W., Ho S., Holmes S.,
 RA Hunt S.E., Jones M.C., Kershaw J., Kimberley A.M., King A.,
 RA Laird G.K., Langford C.F., Leversha M.A., Lloyd C., Lloyd D.M.,
 RA Martyn I.D., Mashreghi-Mohammadi M., Matthews L.H., McCann O.T.,
 RA McClay J., McLaren S., McMurray A.A., Milne S.A., Mortimore B.J.,
 RA Odell C.N., Pavitt R., Pearce A.V., Pearson D., Phillimore B.J.C.T.,
 RA Phillips S.H., Plumb R.W., Ramsay H., Ramsey Y., Rogers L., Ross M.T.,
 RA Scott C.E., Sehra H.K., Skuce C.D., Smalley S., Smith M.L.,
 RA Soderlund C., Spragon L., Steward C.A., Sulston J.E., Swann R.M.,
 RA Vaudin M., Wall M., Wallis J.M., Whiteley M.N., Willey D.L.,
 RA Williams L., Williams S.A., Williamson H., Wilmer T.E., Wilming L.,
 RA Wright C.L., Hubbard T., Bentley D.R., Beck S., Rogers J., Shimizu N.,
 RA Minoshima S., Kawasaki K., Sasaki T., Asakawa S., Kudoh J.,
 RA Shintani A., Shibuya K., Yoshizaki Y., Aoki N., Mitsuyama S.,
 RA Roe B.A., Chen F., Chu L., Crabtree J., Deschamps S., Do A., Do T.,
 RA Dorman A., Fang F., Fu Y., Hu P., Hua A., Kenton S., Lai H., Lao H.I.,
 RA Lewis J., Lewis S., Lin S.-P., Loh P., Malaj E., Nguyen T., Pan H.,
 RA Phan S., Qi S., Qian Y., Ray L., Ren Q., Shaul S., Sloan D., Song L.,
 RA Wang Q., Wang Y., Wang Z., White J., Willingham D., Wu H., Yao Z.,
 RA Zhan M., Zhang G., Chissole S., Murray J., Miller N., Minx P.,
 RA Fulton R., Johnson D., Bemis G., Bentley D., Bradshaw H., Bourne S.,
 RA Cordes M., Du Z., Fulton L., Goela D., Graves T., Hawkins J.,
 RA Hinds K., Kemp K., Latreille P., Layman D., Ozersky P., Rohlffing T.,
 RA Scheet P., Walker C., Wamsley A., Wohldmann P., Pepin K., Nelson J.,
 RA Korf I., Bedell J.A., Hillier L., Mardis E., Waterston R., Wilson R.,

RA Emanuel B.S., Shaikh T., Kurahashi H., Saitta S., Budarf M.L.,
 RA McDermid H.E., Johnson A., Wong A.C.C., Morrow B.E., Edelmann L.,
 RA Kim U.J., Shizuya H., Simon M.I., Dumanski J.P., Peyrard M., Kedra D.,
 RA Seroussi E., Fransson I., Tapia I., Bruder C.E., O'Brien K.P.,
 RA Wilkinson P., Bodenteich A., Hartman K., Hu X., Khan A.S., Lane L.,
 RA Tilahun Y., Wright H.;
 RT "The DNA sequence of human chromosome 22.";
 RL Nature 402:489-495(1999).
 RN [6]
 RP SEQUENCE FROM N.A. (ISOFORM C).
 RC TISSUE=Brain;
 RX MEDLINE=22388257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [7]
 RP SEQUENCE OF 1-26 FROM N.A.
 RX PubMed=11829738;
 RA Castoldi M., Chu M.-L.;
 RT "Structural and functional characterization of the human and mouse
 RT fibulin-1 gene promoters: role of Sp1 and Sp3.";
 RL Biochem. J. 362:41-50(2002).
 RN [8]
 RP SEQUENCE OF 30-44.
 RX MEDLINE=89354537; PubMed=2527614;
 RA Argraves W.S., Dickerson K., Burgess W.H., Ruoslahti E.;
 RT "Fibulin, a novel protein that interacts with the fibronectin
 RT receptor beta subunit cytoplasmic domain.";
 RL Cell 58:623-629(1989).
 RN [9]
 RP SELF-ASSOCIATION AND INTERACTION WITH FN1.
 RX PubMed=1400330;
 RA Balbona K., Tran H., Godyna S., Ingham K.C., Strickland D.K.,
 RA Argraves W.S.;
 RT "Fibulin binds to itself and to the carboxyl-terminal heparin-binding
 RT region of fibronectin.";
 RL J. Biol. Chem. 267:20120-20125(1992).
 RN [10]
 RP POSSIBLE FUNCTION.
 RX PubMed=7534784;

RA Roark E.F., Keene D.R., Haudenschild C.C., Godyna S., Little C.D.,
 RA Argraves W.S.;
 RT "The association of human fibulin-1 with elastic fibers: an
 RT immunohistological, ultrastructural, and RNA study.";
 RL J. Histochem. Cytochem. 43:401-411(1995).
 RN [11]
 RP INTERACTION WITH FGB.
 RX PubMed=7642629;
 RA Tran H., Tanaka A., Litvinovich S.V., Medved L.V., Haudenschild C.C.,
 RA Argraves W.S.;
 RT "The interaction of fibulin-1 with fibrinogen. A potential role in
 RT hemostasis and thrombosis.";
 RL J. Biol. Chem. 270:19458-19464(1995).
 RN [12]
 RP DEVELOPMENTAL STAGE.
 RX PubMed=8737292;
 RA Miosge N., Gotz W., Sasaki T., Chu M.-L., Timpl R., Herken R.;
 RT "The extracellular matrix proteins fibulin-1 and fibulin-2 in the
 RT early human embryo.";
 RL Histochem. J. 28:109-116(1996).
 RN [13]
 RP INDUCTION.
 RX MEDLINE=96133928; PubMed=8552629;
 RA Clinton G.M., Rougeot C., Derancourt J., Roger P., Defrenne A.,
 RA Godyna S., Argraves W.S., Rochefort H.;
 RT "Estrogens increase the expression of fibulin-1, an extracellular
 RT matrix protein secreted by human ovarian cancer cells.";
 RL Proc. Natl. Acad. Sci. U.S.A. 93:316-320(1996).
 RN [14]
 RP CALCIUM, SELF-ASSOCIATION, AND FN1-BINDING SITES.
 RX PubMed=9278415;
 RA Tran H., VanDusen W.J., Argraves W.S.;
 RT "The self-association and fibronectin-binding sites of fibulin-1 map
 RT to calcium-binding epidermal growth factor-like domains.";
 RL J. Biol. Chem. 272:22600-22606(1997).
 RN [15]
 RP ROLE IN TUMOR FORMATION AND INVASION.
 RX PubMed=9393974;
 RA Qing J., Maher V.M., Tran H., Argraves W.S., Dunstan R.W.,
 RA McCormick J.J.;
 RT "Suppression of anchorage-independent growth and matrigel invasion and
 RT delayed tumor formation by elevated expression of fibulin-1D in human
 RT fibrosarcoma-derived cell lines.";
 RL Oncogene 15:2159-2168(1997).
 RN [16]
 RP INDUCTION.
 RX PubMed=9811350;
 RA Roger P., Pujol P., Lucas A., Baldet P., Rochefort H.;
 RT "Increased immunostaining of fibulin-1, an estrogen-regulated protein
 RT in the stroma of human ovarian epithelial tumors.";
 RL Am. J. Pathol. 153:1579-1588(1998).
 RN [17]
 RP ROLE IN TUMOR FORMATION AND INVASION.
 RX PubMed=9466671;
 RA Hayashido Y., Lucas A., Rougeot C., Godyna S., Argraves W.S.,
 RA Rochefort H.;
 RT "Estradiol and fibulin-1 inhibit motility of human ovarian- and

RT breast-cancer cells induced by fibronectin.";
 RL Int. J. Cancer 75:654-658(1998).
 RN [18]
 RP INTERACTION WITH NOV.
 RX PubMed=9927660;
 RA Perbal B., Martinerie C., Sainson R., Werner M., He B., Roizman B.;
 RT "The C-terminal domain of the regulatory protein NOVH is sufficient to

Query Match 29.1%; Score 700; DB 1; Length 703;
 Best Local Similarity 34.7%; Pred. No. 8.1e-45;
 Matches 160; Conservative 65; Mismatches 148; Indels 88; Gaps 21;

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Qy      1 QCTNGFDLDRQSGQCLDIDECRTIPEACRGDMMCVNQNGGYLCIPRTNPVYRGPYSNPYS 60
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Db      293 QCKSGFIQD-ALGNCIDINECLSIAPCPIGHTCINTEGSYTC----- 334

Qy      61 TPYSGPYPAAPPLSAPNYPTISRPLICRFGYQM-DESNQCVDVDECATDSHCNPTQIC 119
      : || | | | | | | | | | | | | | |
Db      335 -----QKNVPN-----CGRGYHLNEEGTRCVDVDECAPPAEPCGKGHRC 373

Qy      120 INTEGGYTCSDTDGYWL--LEGQCLDIDEC-RY--GYCQQLCANVPGSYSCTCNPGFTLN 174
      :|: | : | | | | : | :|:| | | | | | | | | | | |
Db      374 VNSPGSFRCECKTGYYFDGISRMCVDVNECQRYPGRLCGHKCENTLGSYLCSCSVGFRLS 433

Qy      175 EDGRSCQDVNECATENPCVQTCVNTYGSFICRCDPGYELEE-DGVHCSDMDECSF--SEF 231
      |||||:|:|:|:|:|:| | | | | | | | | | | | | |
Db      434 VDGRSCEDINECSS-SPCSQECANVYGSYQCYCRRGYQLSDVDGVTCEDIDECALPTGGH 492

Qy      232 LCQHECVNQPGTYFCSCP-PGYILLDDNRSCQDINECEHRNHTCNLQQTTCYNLQGGFKCI 290
      :| : | :| | | :| | | | | | | | | | | | | | | |
Db      493 ICSYRCINIPGSFQCSCPSSGYYRLAPNGRNCQDIDECVTGIHNCSINETCFNIQGGFRCL 552

Qy      291 DPIRCEEPYLRISDN-----RCMCPAENPGCRDQPFTILYRDMDVVSGRSV----- 336
      | | | | : | | | | | | | | | | | | | | | |
Db      553 -AFCEPENYRRSAATLQQEKTDTVRCI-----KSCRPNDVTCVFDPVHTISHTVISLPTF 606

Qy      337 -----PADIFQMQA-TTRYPG--AAYIFQIKSGNEGREF-----YMRQTGPISATLVMTR 383
      | : | :| | | :| | | | | | | | | | | | | | |
Db      607 REFTRPEEIIIFLRAITPPHPASQANIIFDITEGNLRDSFDIIKRYM--DGMTVGVVVRQVR 664

Qy      384 PIKGPREIQLDLEM-ITVNTVINFRGSSVIRLRIYVSQYPF 423
      || || | || | | | :| :| :|:| | | | |
Db      665 PIVGPFHAVLKLEMNYVVGGVVSHR--NVNVNRI FVSEYWF 703
  
```

RESULT 14

FBL1_MOUSE

ID FBL1_MOUSE STANDARD; PRT; 705 AA.
 AC Q08879; Q08878; Q8C3B1; Q91ZC9; Q922K8;
 DT 01-OCT-1994 (Rel. 30, Created)
 DT 15-SEP-2003 (Rel. 42, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Fibulin-1 precursor (Basement-membrane protein 90) (BM-90).
 GN FBLN1.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A. (ISOFORMS C AND D), AND LIGANDS INTERACTION.
 RX MEDLINE=93358897; PubMed=8354280;
 RA Pan T.-C., Kluge M., Zhang R.Z., Mayer U., Timpl R., Chu M.-L.;
 RT "Sequence of extracellular mouse protein BM-90/fibulin and its
 RT calcium-dependent binding to other basement-membrane ligands.";
 RL Eur. J. Biochem. 215:733-740(1993).
 RN [2]
 RP SEQUENCE FROM N.A. (ISOFORM C).
 RC STRAIN=C57BL/6J; TISSUE=Head, and Urinary bladder;
 RX MEDLINE=22354683; PubMed=12466851;
 RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
 RA Nikaido I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,
 RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,
 RA Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
 RA Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,
 RA Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S.,
 RA Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,
 RA Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,
 RA Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,
 RA Kanai A., Kawaji H., Kawasaki Y., Kedzierski R.M., King B.L.,
 RA Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
 RA Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,
 RA Nagashima T., Numata K., Okido T., Pavan W.J., Pertea G., Pesole G.,
 RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,
 RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
 RA Sandelin A., Schneider C., Semple C.A., Setou M., Shimada K.,
 RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,
 RA Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,
 RA Wilming L.G., Wynshaw-Boris A., Yanagisawa M., Yang I., Yang L.,
 RA Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,
 RA Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,
 RA Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,
 RA Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,
 RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,
 RA Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
 RA Birney E., Hayashizaki Y.;
 RT "Analysis of the mouse transcriptome based on functional annotation of
 RT 60,770 full-length cDNAs.";
 RL Nature 420:563-573(2002).
 RN [3]
 RP SEQUENCE FROM N.A. (ISOFORM C).
 RC TISSUE=Breast tumor;
 RX MEDLINE=22388257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,

RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [4]
 RP SEQUENCE OF 1-26 FROM N.A.
 RX PubMed=11829738;
 RA Castoldi M., Chu M.-L.;
 RT "Structural and functional characterization of the human and mouse
 RT fibulin-1 gene promoters: role of Sp1 and Sp3.";
 RL Biochem. J. 362:41-50(2002).
 RN [5]
 RP CHARACTERIZATION OF NID AFFINITY.
 RX PubMed=7844816;
 RA Sasaki T., Kostka G., Goehring W., Wiedemann H., Mann K., Chu M.-L.,
 RA Timpl R.;
 RT "Structural characterization of two variants of fibulin-1 that differ
 RT in nidogen affinity.";
 RL J. Mol. Biol. 245:241-250(1995).
 RN [6]
 RP DEVELOPMENTAL STAGE.
 RX PubMed=8850569;
 RA Zhang H.-Y., Timpl R., Sasaki T., Chu M.-L., Ekblom P.;
 RT "Fibulin-1 and fibulin-2 expression during organogenesis in the
 RT developing mouse embryo.";
 RL Dev. Dyn. 205:348-364(1996).
 RN [7]
 RP NID-BINDING SITE.
 RC STRAIN=129/Sv;
 RX PubMed=9299350;
 RA Adam S., Goehring W., Wiedemann H., Chu M.-L., Timpl R., Kostka G.;
 RT "Binding of fibulin-1 to nidogen depends on its C-terminal globular
 RT domain and a specific array of calcium-binding epidermal growth
 RT factor-like (EG) modules.";
 RL J. Mol. Biol. 272:226-236(1997).
 RN [8]
 RP BINDING TO LAMA2.
 RX PubMed=10022829;
 RA Talts J.F., Andac Z., Goehring W., Brancaccio A., Timpl R.;
 RT "Binding of the G domains of laminin alpha1 and alpha2 chains and
 RT perlecan to heparin, sulfatides, alpha-dystroglycan and several
 RT extracellular matrix proteins.";
 RL EMBO J. 18:863-870(1999).
 RN [9]
 RP INTERACTION WITH AGC1 AND CSPG2.
 RX PubMed=10400671;
 RA Asperberg A., Adam S., Kostka G., Timpl R., Heinegaard D.;
 RT "Fibulin-1 is a ligand for the C-type lectin domains of aggrecan and
 RT versican.";
 RL J. Biol. Chem. 274:20444-20449(1999).
 RN [10]
 RP INTERACTION WITH NID.
 RX PubMed=11589703;

RA Ries A., Goehring W., Fox J.W., Timpl R., Sasaki T.;
 RT "Recombinant domains of mouse nidogen-1 and their binding to basement
 RT membrane proteins and monoclonal antibodies.";
 RL Eur. J. Biochem. 268:5119-5128(2001).
 RN [11]
 RP DOWN-REGULATION BY GLUCOCORTICOIDS.
 RX PubMed=11737251;
 RA Gu Y.-C., Talts J.F., Gullberg D., Timpl R., Ekblom M.;
 RT "Glucocorticoids down-regulate the extracellular matrix proteins
 RT fibronectin, fibulin-1 and fibulin-2 in bone marrow stroma.";
 RL Eur. J. Haematol. 67:176-184(2001).
 RN [12]
 RP TISSUE SPECIFICITY, AND DEVELOPMENTAL STAGE.
 RX PubMed=11238726;
 RA Ohsawa I., Takamura C., Kohsaka S.;
 RT "Fibulin-1 binds the amino-terminal head of beta-amyloid precursor
 RT protein and modulates its physiological function.";
 RL J. Neurochem. 76:1411-1420(2001).
 RN [13]
 RP INTERACTION WITH E6, AND INHIBITION OF E6-MEDIATED TRANSFORMATION.
 RX PubMed=12200142;
 RA Du M., Fan X., Hong E., Chen J.J.;
 RT "Interaction of oncogenic papillomavirus E6 proteins with fibulin-1.";
 RL Biochem. Biophys. Res. Commun. 296:962-969(2002).
 RN [14]
 RP DEVELOPMENTAL STAGE.
 RX PubMed=11836357;
 RA Debeer P., Schoenmakers E.F.P.M., Twal W.O., Argraves W.S.,
 RA De Smet L., Fryns J.-P., Van De Ven W.J.M.;
 RT "The fibulin-1 gene (FBLN1) is disrupted in a t(12;22) associated with
 RT a complex type of synpolydactyly.";
 RL J. Med. Genet. 39:98-104(2002).
 CC -!- FUNCTION: Incorporated into fibronectin-containing matrix fibers.
 CC May play a role in cell adhesion and migration along protein
 CC fibers within the extracellular matrix (ECM). Could be important
 CC for certain developmental processes and contribute to the
 CC supramolecular organization of ECM architecture, in particular to
 CC those of basement membranes.
 CC -!- SUBUNIT: Interacts with itself and with various extracellular
 CC matrix components such as FN1, LAMA1, LMA2, NID, AGC1, CSPG2 and
 CC type IV collagen. Interacts also with papillomavirus E6 proteins.
 CC Binding analysis demonstrated for isoform C a 100-fold stronger
 CC binding to the basement membrane protein NID than for isoform D.
 CC -!- SUBCELLULAR LOCATION: Secreted; extracellular matrix.
 CC -!- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=4;
 CC Name=D;
 CC IsoId=Q08879-1; Sequence=Displayed;
 CC Name=A;
 CC IsoId=Q08879-3; Sequence=Not described;
 CC Name=B;
 CC IsoId=Q08879-4; Sequence=Not described;
 CC Name=C;
 CC IsoId=Q08879-2; Sequence=VSP_001386;
 CC Note=Conflict E -> A at position 571 of isoform C (Ref.1);
 CC -!- TISSUE SPECIFICITY: Detected in most organs (brain, heart, lung,
 CC spleen, liver and kidney). Neurons are the predominant source of

CC production in the brain. Not expressed significantly by astrocytes
 CC or microglia.
 CC -!- DEVELOPMENTAL STAGE: The differential expression of the fibulin
 CC family contributes to the formation of molecularly distinct
 CC extracellular matrices already during early developmental stages
 CC of a large number of tissues. Increase expression at neonate stage
 CC in the brain. Expressed in interdigital regions of the handplate
 CC of a 12 dpc embryo and in the lateral perichondrial region.
 CC Similar expression persists in the 13 dpc handplate particularly
 CC in the perichondrial regions and apical aspects of the developing
 CC digits.
 CC -!- INDUCTION: Glucocorticoids suppressed mRNA expression and protein
 CC synthesis.
 CC -!- SIMILARITY: Belongs to the fibulin family.
 CC -!- SIMILARITY: Contains 3 anaphylatoxin-like domains.
 CC -!- SIMILARITY: Contains 9 EGF-like domains.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -

Query Match 29.0%; Score 699; DB 1; Length 705;
 Best Local Similarity 35.0%; Pred. No. 9.6e-45;
 Matches 159; Conservative 67; Mismatches 154; Indels 74; Gaps 21;

```

Qy      1 QCTNGFDLDRQSGQCLDIDECRTIPEACRGDMMCVNQNGGYLCIPRTNPVYRGPYSNPYS 60
      ||:||| | | |:||:| | | | | | | | | |
Db      295 QCKSGFIQD-ALGNCIDINECLSIAPCPVGQTCINTEGSYTC----- 336

Qy      61 TPYSGPYAAPPLSAPNYPTISRPLICRFGYQM-DESNQCVDVDECATDSHCNPTQIC 119
      : || | | | | | | | | | | | | | |
Db      337 -----QKNVFN-----CGRGYHLNEEGTRCVDVDECSPPAEPCKGHHHC 375

Qy     120 INTEGGYTCSTDGYWL--LEGQCLDIDEC-RY--GYCQQLCANVPGSYSCTCNPGFTLN 174
      :|: | : | | | : | :|:| | | | | | | | | | | |
Db     376 LNSPGSFRCECKAGFYFDGISRTCDINECQRYPGRLCGHKCENTPGSFHCSCSAGFRLS 435

Qy     175 EDGRSCQDVNECATENPCVQTCVNTYGSFICRCDPGYELEE-DGVHCSMDDECSF--SEF 231
      |||||:|||| | | | | | | | | | | | | | | |
Db     436 VDGRSCEDVNEC-LNSPCSQECANVYGSYQCYCRRGYQLSDVDGVTCEIDICALPTGGH 494

Qy     232 LCQHECVNQPGTYFCSCP-PGYILLDDNRSCQDINECEHRNHTCNLQQTTCYNLQGGFKCI 290
      :| : | : | | | | | | | | | | | | | | | | |
Db     495 ICSYRCINIPGSFQCSCPSSGYRLAPNGRNCQDIDECVTGIHNCSINETCFNIQGSFRCL 554

Qy     291 DPIRCEEPYLRISDN-----RCM--CPAENPGC-RDQPFTILYRDMDVVSGRSV-- 336
      | | | | : | | | | | | | | | | | | | | |
Db     555 S-FECPENYRRSADTFRQEKTDTVRCIKSCRPNDEACVRDPVHTVSHTVISLPTFREFT 613

Qy     337 PADIFQMATT-RYPG--AYYIFQIKSGNEGREFYM---RQTGPISATLVMTRPIKGP 390
      | : | : | | | | | | | | | | | | | | | |
Db     614 PEEIIFLRAVTPLYPANQADIIFDITEGNLRDSFDIIKRYEDGMTVGTVVRQVRPIVGP 673

Qy     391 IQLDLEM-ITVNTVINFRGSSVIRLRIYVSQYPF 423
      | | | | : | : | : | : | : | : |
Db     674 AVLKLEMNYVLGGVVSHR--NVVNVHIFVSEYWF 705

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RESULT 15

FBL1_BRARE

ID FBL1_BRARE STANDARD; PRT; 681 AA.
AC O42182; O42183;
DT 15-SEP-2003 (Rel. 42, Created)
DT 15-SEP-2003 (Rel. 42, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Fibulin-1 precursor.
GN FBLN1.
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORMS C AND D).
RA Zhang H.-Y., Lardelli M., Ekblom P.;
RT "Sequence of zebrafish fibulin-1 and its expression in developing
RT heart and other embryonic organs.";
RL Dev. Genes Evol. 207:340-351(1997).
CC -!- FUNCTION: Incorporated into fibronectin-containing matrix fibers.
CC May play a role in cell adhesion and migration along protein
CC fibers within the extracellular matrix (ECM). Could be important
CC for certain developmental processes and contribute to the
CC supramolecular organization of ECM architecture, in particular to
CC those of basement membranes.
CC -!- SUBUNIT: Interacts with itself and with various extracellular
CC matrix components such as FN1, LAMA1, NID, AGC1 and CSPG2.
CC -!- SUBCELLULAR LOCATION: Secreted; extracellular matrix.
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=D;
CC IsoId=O42182-1; Sequence=Displayed;
CC Name=C;
CC IsoId=O42182-2; Sequence=VSP_007379;
CC -!- DEVELOPMENTAL STAGE: Isoform C is detected in the later blastula
CC period, 4 h after fertilization. Isoform D is not detected at this
CC stage, it first appears during the gastrula period in 8-h-old
CC embryos. Expression of both isoforms is then maintained throughout
CC development. During later developmental stages, prominent
CC expression is seen in regions where tissue compartments are
CC continuously moving in relation to each other.
CC -!- SIMILARITY: Belongs to the fibulin family.
CC -!- SIMILARITY: Contains 3 anaphylatoxin-like domains.
CC -!- SIMILARITY: Contains 9 EGF-like domains.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; AF013751; AAB80944.1; -.
DR EMBL; AF013752; AAB80945.1; -.
DR HSSP; P35555; 1EMN.

DR ZFIN; ZDB-GENE-990415-73; fb1n1.
 DR InterPro; IPR000020; Anaphylatoxin.
 DR InterPro; IPR000152; Asx_hydroxyl.
 DR InterPro; IPR001881; EGF_Ca.
 DR InterPro; IPR006209; EGF_like.
 DR InterPro; IPR001673; S_mold_repeat.
 DR Pfam; PF01821; ANATO; 1.
 DR Pfam; PF00008; EGF; 4.
 DR SMART; SM00104; ANATO; 2.
 DR SMART; SM00179; EGF_CA; 5.
 DR PROSITE; PS01177; ANAPHYLATOXIN_1; 1.
 DR PROSITE; PS01178; ANAPHYLATOXIN_2; 1.
 DR PROSITE; PS00010; ASX_HYDROXYL; 3.
 DR PROSITE; PS01186; EGF_2; 3.
 DR PROSITE; PS01187; EGF_CA; 6.
 KW Signal; Alternative splicing; Glycoprotein; Extracellular matrix;
 KW Repeat; EGF-like domain; Calcium-binding.
 FT SIGNAL 1 17 POTENTIAL.
 FT CHAIN 18 681 FIBULIN-1.
 FT DOMAIN 29 63 ANAPHYLATOXIN-LIKE 1.
 FT DOMAIN 68 107 ANAPHYLATOXIN-LIKE 2.
 FT DOMAIN 108 139 ANAPHYLATOXIN-LIKE 3.
 FT DOMAIN 158 192 EGF-LIKE 1.
 FT DOMAIN 193 238 EGF-LIKE 2, CALCIUM-BINDING (POTENTIAL).
 FT DOMAIN 239 284 EGF-LIKE 3, CALCIUM-BINDING (POTENTIAL).
 FT DOMAIN 285 331 EGF-LIKE 4, CALCIUM-BINDING (POTENTIAL).
 FT DOMAIN 332 373 EGF-LIKE 5, CALCIUM-BINDING (POTENTIAL).
 FT DOMAIN 374 415 EGF-LIKE 6, CALCIUM-BINDING (POTENTIAL).
 FT DOMAIN 416 455 EGF-LIKE 7, CALCIUM-BINDING (POTENTIAL).
 FT DOMAIN 456 499 EGF-LIKE 8, CALCIUM-BINDING (POTENTIAL).
 FT DOMAIN 500 554 EGF-LIKE 9, CALCIUM-BINDING (POTENTIAL).
 FT DISULFID 29 55 BY SIMILARITY.
 FT DISULFID 30 62 BY SIMILARITY.
 FT DISULFID 43 63 BY SIMILARITY.
 FT DISULFID 72 103 BY SIMILARITY.
 FT DISULFID 85 104 BY SIMILARITY.
 FT DISULFID 106 125 BY SIMILARITY.
 FT DISULFID 107 138 BY SIMILARITY.
 FT DISULFID 114 139 BY SIMILARITY.
 FT DISULFID 162 171 BY SIMILARITY.
 FT DISULFID 167 176 BY SIMILARITY.
 FT DISULFID 178 191 BY SIMILARITY.
 FT DISULFID 197 210 BY SIMILARITY.
 FT DISULFID 204 219 BY SIMILARITY.
 FT DISULFID 225 237 BY SIMILARITY.
 FT DISULFID 243 256 BY SIMILARITY.
 FT DISULFID 250 265 BY SIMILARITY.
 FT DISULFID 271 283 BY SIMILARITY.
 FT DISULFID 289 301 BY SIMILARITY.
 FT DISULFID 317 330 BY SIMILARITY.
 FT DISULFID 336 348 BY SIMILARITY.
 FT DISULFID 343 357 BY SIMILARITY.
 FT DISULFID 359 372 BY SIMILARITY.
 FT DISULFID 378 390 BY SIMILARITY.
 FT DISULFID 386 399 BY SIMILARITY.
 FT DISULFID 401 414 BY SIMILARITY.
 FT DISULFID 420 429 BY SIMILARITY.

FT DISULFID 440 454 BY SIMILARITY.
 FT DISULFID 460 473 BY SIMILARITY.
 FT DISULFID 469 482 BY SIMILARITY.
 FT DISULFID 484 498 BY SIMILARITY.
 FT DISULFID 504 517 BY SIMILARITY.
 FT DISULFID 511 526 BY SIMILARITY.
 FT DISULFID 531 553 BY SIMILARITY.
 FT CARBOHYD 173 173 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT VARSPLIC 542 681 RPRVDRADIIRCVKSCQHNDISCVLNPILSHSHTAISLPTF
 FT REFNKPEEIVFLRSPTPTHLPHMDSPEIVYDILEGNIQNSF
 FT DIIKRLDHGMIVGVVKQVRPLVGPVRTVLKCLAMNYVTNGVV
 FT SHRNIINVRIYVSEFWF -> RCERLSCNESNECMAFTRRI
 FT TYYQLTFPAKIPVPTDLFRMGPSNTALGDDIEVAIVDGNRD
 FT GFFAAKRLDHGGVLVLQKPIAWPQDFQIALEMKLKRFHLS
 FT IYLFKIRPVRHARRHQQR (in isoform C).
 FT /FTId=VSP_007379.
 SQ SEQUENCE 681 AA; 74459 MW; 175C966305A46699 CRC64;

Query Match 26.2%; Score 629.5; DB 1; Length 681;
 Best Local Similarity 32.8%; Pred. No. 1.3e-39;
 Matches 151; Conservative 64; Mismatches 160; Indels 85; Gaps 21;

Qy 1 QCTNGFDLDRQSGQCLDIDECRTIPEACRGDMMCVNQNGGYLCIPRTNPVYRGPYSNPYS 60
 || || | | :||:| :| || | | :| :
 Db 270 QCAAGFIQD-ALGSCIDINECVSVTALSRLG-QMCFNTVGSFICQRHS----- 314

 Qy 61 TPYSGPYPAAPPLSAPNYPTISRPLICRFGYQMD-ESNQCVDVDECATDSHCNPTQIC 119
 : | || :| :|||:|||| :| :|
 Db 315 -----VTCGRGYHLNAEGTRCVDIDECAGPDNSCD-GHGC 348

 Qy 120 INTEGgyTCsCTDGYWL--LEGQCLDIDECRYGY---CQQLCANVPGSYsCTCNPGFTL 173
 || | | | | : : | | | | | | | | : | | | | :| || |
 Db 349 INLVGSYRCECRTGFI FNSISRSCEDIDECR-NYPGRLLCAHKCENILGSYKCSCTAGFKL 407

 Qy 174 NEDGRSCQDVNECATENPCVQTCVNTYGSFICRCDPGYELEE-DGVHCSMDDECSF--SE 230
 : |||:| |||| : :|| | | |||: | ||:| : ||: | |:|||:
 Db 408 ADDGRNCDDVNECES-SPCSQGCANVYGSYQSYCRRGYQLSDADGITCEDIDECALPTGG 466

 Qy 231 FLCQHECVNQPGTYFCSCP-PGYILLDDNRSCQDINECEHRNHTCNLQQTTCYNLQGGFKC 289
 : | : | | ||:| :|| | | : |||||:| | :| : :| :| |||:|
 Db 467 HICSYRCHNTPGSFHCTCPASGYTLAANGRSCQDIDECLEGTGTHSCSESESCFNIQGGFRC 526

 Qy 290 IDPIRCEEPLYLRISDN-----RCM--CPAENPGCRDQPFTILYRDMDVVS----- 332
 : | | | | ||:| : | | | | :|
 Db 527 LS-FDCPANYRRSGDTRPRVDRADIIRCVKSCQHNDISCVLNP--ILSHSHTAISLPTFR 583

 Qy 333 GRSVPADIFQMATT-----RYPGAYYIFQIKSGNEGREFYMRQT---GPISATLVMTRP 384
 : | :| :|| :| :| || :| :| :| :| :| :|
 Db 584 EFNKPEEIVFLRSPTPTHLPHMDSPEIVYDILEGNIQNSFDIIKRLDHGMIVGVVKQVRP 643

 Qy 385 IKGPREIQLDLEM-ITVNTVINFRGSSVIRLRIYVSQYPF 423
 : || | | | | :|| :| :|||:| :|
 Db 644 LVGPVRTVLKCLAMNYVTNGVVSHR--NIINVRIYVSEFWF 681

Search completed: January 9, 2004, 12:34:07
 Job time : 11.713 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: January 9, 2004, 12:32:07 ; Search time 32.5385 Seconds
(without alignments)
3354.684 Million cell updates/sec

Title: US-09-674-379A-14
Perfect score: 2407
Sequence: 1 QCTNGFDLDRQSGQCLDIDE.....INFRGSSVIRLRIYVSQYPF 423

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL_23:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_rvirus:*
16: sp_bacteriap:*
17: sp_archeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	%	Query				
No.	Score	Match Length	DB	ID		Description

1	1276.5	53.0	443	4	Q96TF5	Q96tf5 homo sapien
2	1273.5	52.9	443	11	Q9JM06	Q9jm06 mus musculu
3	1253.5	52.1	443	4	Q9H3D5	Q9h3d5 homo sapien
4	1096.5	45.6	493	11	Q8BPB5	Q8bpb5 mus musculu
5	960.5	39.9	387	11	Q8K0J4	Q8k0j4 mus musculu
6	741.5	30.8	685	11	Q922K8	Q922k8 mus musculu
7	741.5	30.8	685	11	Q8C3B1	Q8c3b1 mus musculu
8	735.5	30.6	683	4	Q8TBH8	Q8tbh8 homo sapien
9	731.5	30.4	1174	11	Q99K58	Q99k58 mus musculu
10	721	30.0	598	6	Q8MJJ9	Q8mjj9 cercopithec
11	713	29.6	704	13	O73774	O73774 gallus gall
12	703.5	29.2	576	4	Q9Y3V7	Q9y3v7 homo sapien
13	702.5	29.2	1231	4	Q8IUI1	Q8iui1 homo sapien
14	701.5	29.1	1231	4	Q8IUI0	Q8iui0 homo sapien
15	695	28.9	638	4	Q8NBH6	Q8nbh6 homo sapien
16	674.5	28.0	495	4	Q9HBQ5	Q9hbq5 homo sapien
17	629.5	26.2	681	13	O42182	O42182 brachydanio
18	587	24.4	698	5	Q9V4B8	Q9v4b8 drosophila
19	581.5	24.2	554	4	Q9UH16	Q9uh16 homo sapien
20	547.5	22.7	1409	5	Q9VS89	Q9vs89 drosophila
21	542	22.5	2673	4	Q96SC3	Q96sc3 homo sapien
22	531	22.1	5636	4	Q96RW7	Q96rw7 homo sapien
23	518.5	21.5	2872	11	Q9WUH8	Q9wuh8 rattus norv
24	517.5	21.5	741	4	Q96K89	Q96k89 homo sapien
25	516.5	21.5	1398	13	Q8AXM6	Q8axm6 xenopus lae
26	516	21.4	1389	11	Q8CG18	Q8cg18 mus musculu
27	516	21.4	1713	11	Q8CG19	Q8cg19 mus musculu
28	514.5	21.4	1399	13	Q8JFZ4	Q8jfh4 xenopus lae
29	512.5	21.3	3857	11	O88840	O88840 mus musculu
30	512	21.3	1713	11	O88349	O88349 mus musculu
31	511.5	21.3	2809	4	Q96JP8	Q96jp8 homo sapien
32	510.5	21.2	787	11	Q8K061	Q8k061 mus musculu
33	508	21.1	188	11	Q8R1U8	Q8rlu8 mus musculu
34	507.5	21.1	708	13	P87363	P87363 gallus gall
35	506.5	21.0	2906	11	Q9WUH9	Q9wuh9 rattus norv
36	493.5	20.5	729	11	Q8BNH3	Q8bnh3 mus musculu
37	491.5	20.4	937	5	Q9BLJ1	Q9blj1 ciona intes
38	484.5	20.1	1963	6	Q28019	Q28019 bos taurus
39	482.5	20.0	1764	11	O35806	O35806 rattus norv
40	480.5	20.0	517	4	Q9NP01	Q9np01 homo sapien
41	474	19.7	746	4	Q96HB9	Q96hb9 homo sapien
42	474	19.7	893	6	Q8MJK0	Q8mjk0 cercopithec
43	474	19.7	1256	4	Q9NS15	Q9ns15 homo sapien
44	474	19.7	1382	4	Q9H7K2	Q9h7k2 homo sapien
45	471.5	19.6	1095	11	Q60784	Q60784 mus musculu

ALIGNMENTS

RESULT 1

Q96TF5

ID	Q96TF5	PRELIMINARY;	PRT;	443 AA.
AC	Q96TF5;			
DT	01-DEC-2001	(TrEMBLrel. 19, Created)		
DT	01-DEC-2001	(TrEMBLrel. 19, Last sequence update)		
DT	01-MAR-2003	(TrEMBLrel. 23, Last annotation update)		


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Qy      361 GNEGREFYMRQTGPISATLVMTRPIKGPRIQLDLEMITVNTVINFRGSSVIRLRIYVSQ 420
      || :||:|| :|| ||: ||: |||| |||||:|:|:::| |||:| :|
Db      381 GNSQGDFYIRQINNVSAMLVLARPTGPREYVLDLEMTMNSLMSYRASSVLRLTVFVGA 440

Qy      421 YPF 423
      ||
Db      441 YTF 443

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RESULT 2

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Q9JM06
ID   Q9JM06          PRELIMINARY;          PRT;    443 AA.
AC   Q9JM06;
DT   01-OCT-2000 (TrEMBLrel. 15, Created)
DT   01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT   01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE   EGF-containing fibulin-like extracellular matrix protein 2.
GN   EFEMP2.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=20435063; PubMed=10982184;
RA   Katsanis N., Venable S., Smith J.R., Lupski J.R.;
RT   "Isolation of a paralog of the Doyme honeycomb retinal dystrophy gene
RT   from the multiple retinopathy critical region on 11q13.";
RL   Hum. Genet. 106:66-72(2000).
DR   EMBL; AF109122; AAF65189.1; -.
DR   HSSP; P00736; 1APQ.
DR   MGD; MGI:1891209; Efemp2.
DR   InterPro; IPR000152; Asx_hydroxyl.
DR   InterPro; IPR001881; EGF_Ca.
DR   InterPro; IPR006209; EGF_like.
DR   InterPro; IPR001491; Thrbomoduln.
DR   Pfam; PF00008; EGF; 4.
DR   PRINTS; PR00907; THRMBOMODULN.
DR   SMART; SM00179; EGF_CA; 4.
DR   PROSITE; PS00010; ASX_HYDROXYL; 4.
DR   PROSITE; PS01186; EGF_2; 4.
DR   PROSITE; PS01187; EGF_CA; 6.
KW   EGF-like domain; Matrix protein.
SQ   SEQUENCE    443 AA;  49452 MW;  5AEC2A91048B336A CRC64;

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Query Match 52.9%; Score 1273.5; DB 11; Length 443;
Best Local Similarity 52.0%; Pred. No. 4.3e-117;
Matches 220; Conservative 65; Mismatches 121; Indels 17; Gaps 3;

QY 1 QCTNGFDLDRQSGQCLDIIDECRTIPEACRGDMMCVNQNGGYLCIPRTNPVYRGPYSNPYS 60
:||:|::| | | |::|| |||||:|:| |:| |||||:|:| | :
Db 38 ECTDGYEWDADSQHCRDVNECLTIPEACKGEMKCINHYGGYLCLPRSAVINDLHG---- 93

QY 61 TPYSGPYPAAPPLSAPNYPTISRPLICRFGYQMDENQCVDVDECATDShQCNPtQICI 120
|| | || :| | ||: || ||||| | | | :| |
Db 94 ---EGPPPPAA-----HAQQPNPCPGYEPDEQESCVDVDECTOALHDCRPSODCH 141

Qy 121 NTEGGYTCSTCDGYWLLEGQCLDIDECRYGYCQQLCANVPGSYSCTCNPGFTLNEDGRSC 180
| | | : | | | : : | | | | | | | | | : | | | : | | |
Db 142 NLPGSYQCTCPDGYRKIGPECVDIDECRYRYCQHRCVNLPGSFRCQCEPGFQLGPNNRSC 201

Qy 181 QDVNECATENPCVQTCVNTYGSFICRCDPGYELEEDGVHCSMDDECSFSEFLCQHECVNQ 240
| | | | | | | | | : | | : | | | : | | | | | | : | | : | | :
Db 202 VDVNECDMGAPCEQRCFNSYGTFLCRCNQGYELHRDGFSCSDIDECGYSSYLCQYRCVNE 261

Qy 241 PGTYFCSCPPGYILLDDNRSCQDINECEHRNHTCNLQQTTCYNLQGGFKCIDPIRCEEPYL 300
| | : | | | | | | | | | : | | | | | : | | : | | : | | :
Db 262 PGRFSCHCPQGYQLL-ATRLCQDIDECETGAHQCSAQTCVNFHGGYRCVDTNRCVEPYV 320

Qy 301 RISDNRCMCPAENPGCRDQPFITILYRDMDVVSGRSVPADIFQMQAATTRYPGAYYIFQIKS 360
: | | | | : | | | | | : | | : | | : | | : | | : | | : | | :
Db 321 QVSDNRCLCPASNPLCREQPSSIVHRYMSITSERSVPADVFIQIATSVPYPGAYNAFQIRS 380

Qy 361 GNEGREFYMRQTGPISATLVMTRPIKGPRIQLDLEMITVNTVINFRGSSVIRLRIYVSQ 420
| | : | | : | | : | | : | | | | | : | | : | | : | | : | | :
Db 381 GNTQGDFYIRQINNVSAMLVLARPVGTGPREYVLDLEMVTMNSLMSYRASSVLRLTVFVGA 440

Qy 421 YPF 423
| |
Db 441 YTF 443

RESULT 3

Q9H3D5

ID Q9H3D5 PRELIMINARY; PRT; 443 AA..
AC Q9H3D5;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Fibulin-like extracellular matrix protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Seibold S., Marx M.;
RT "Cloning of a new fibulin-like gene."
RL Submitted (JAN-1999) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AF124486; AAG45245.1; -.
DR HSSP; P35555; 1EMN.
DR InterPro; IPR000152; Asx_hydroxyl.
DR InterPro; IPR001881; EGF_Ca.
DR InterPro; IPR006209; EGF_like.
DR InterPro; IPR001491; Thrbomoduln.
DR Pfam; PF00008; EGF; 3.
DR PRINTS; PR00907; THRMBOMODULN.
DR SMART; SM00179; EGF_CA; 4.
DR PROSITE; PS00010; ASX_HYDROXYL; 4.
DR PROSITE; PS01186; EGF_2; 4.
DR PROSITE; PS01187; EGF_CA; 5.
KW EGF-like domain; Matrix protein.
SQ SEQUENCE 443 AA; 49535 MW; D91784BF36A8A060 CRC64;

Query Match 52.1%; Score 1253.5; DB 4; Length 443;
 Best Local Similarity 51.3%; Pred. No. 4e-115;
 Matches 217; Conservative 67; Mismatches 122; Indels 17; Gaps 4;

```

Qy      1 QCTNGFDLDRQSGQCLDIDECRTIPEACRGDMMCVNQNGGYLCIPRTNPVYRGPYSNPYS 60
      :||:|::| | | |::|| |||||:|:| |:| |||||:|:| | :
Db      38 ECTDGYEWDPSQHCRDVNECLTIPEACKGEMKCINHYGGYLCLPRSAAVINDLHG---- 93

Qy      61 TPYSGPYPAAPPLSAPNYPTISRPLICRFGYQMDESNQCVDVDECATDSHCNPTQICI 120
      || | || | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      94 ---EGP-PPPVPPAQHPN-----PCPPGYEPDDQDSCVDVDECAQALHRRPSQDCH 141

Qy     121 NTEGGYTCSTDGYWLLEGQCLDIDECRYGYCQQLCANVPGSYSCTCNPGFTLNEDGRSC 180
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db     142 NLSGSYQCTCPDGYRKIGPECVDIDECRYRYCQHRCVNLPGSFRCQCEPGFQLGPNRNSC 201

Qy     181 QDVNECATENPCVQTCVNTYGSFICRCDPGYELEEDGVHCSDMDECSFSEFLCQHECVNQ 240
      ||||| | | | | | | | | | | | | | | | | | | | | | | | | | |
Db     202 VDVNECDMGAPCEQRCFNSYGTFLCRCHQGYELHRDGFSCSDIDECSSYSSYLCQYRCVNE 261

Qy     241 PGTYFCSCPPGYILLDDNRSCQDINECEHRNHTCNLQQTTCYNLQGGFKCIDPIRCEEPYL 300
      || : | | | | | | | | | | | | | | | | | | | | | | | | | |
Db     262 PGRFSCHCPQGYQLL-ATRLCQDIDECESGAHQCEAQTCVNFHGGYRCVDTNRCVEPYI 320

Qy     301 RISDNRCMCPAENPGCRDQPFITILYRDMDVVSGRSVPADIFQMQATTRYPGAYYIFQIKS 360
      ::|:|||:| | | | | | | | | | | | | | | | | | | | | | | |
Db     321 QVSENRLCPASNPLCREQPSSIVHRYMTITSERMRPADVFQIQATSVYPGAYNAFQIRA 380

Qy     361 GNEGREFYMRQTGPISATLVMTRPIKGPREIQLDLEMITVNTVINFRGSSVIRLRIYVSQ 420
      || : ||:| | : | | | | | | | | | | | | | | | | | | | | |
Db     381 GNSQGDFYIRQINNVSAMLVLARPVTGPREYVLDLEMTMNSLMSYRASSVLRLTVFVGA 440

Qy     421 YPF 423
      | |
Db     441 YTF 443
  
```

RESULT 4

Q8BPB5

ID Q8BPB5 PRELIMINARY; PRT; 493 AA.
 AC Q8BPB5;
 DT 01-MAR-2003 (TrEMBLrel. 23, Created)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE Epidermal growth factor-containing fibulin-like extracellular matrix
 DE protein 1.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Xiphoid cartilage;
 RX MEDLINE=22354683; PubMed=12466851;
 RA The FANTOM Consortium,
 RA the RIKEN Genome Exploration Research Group Phase I & II Team;
 RT "Analysis of the mouse transcriptome based on functional annotation of

RA Strausberg R.;
 RL Submitted (JUN-2002) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; BC031184; AAH31184.1; -.
 DR InterPro; IPR000152; Asx_hydroxyl.
 DR InterPro; IPR001881; EGF_Ca.
 DR InterPro; IPR006209; EGF_like.
 DR InterPro; IPR006210; IEGF.
 DR Pfam; PF00008; EGF; 3.
 DR SMART; SM00181; EGF; 5.
 DR SMART; SM00179; EGF_CA; 5.
 DR PROSITE; PS00010; ASX_HYDROXYL; 4.
 DR PROSITE; PS01186; EGF_2; 4.
 DR PROSITE; PS01187; EGF_CA; 5.
 KW Hypothetical protein.
 SQ SEQUENCE 387 AA; 43334 MW; EE88DC9D1422C1C7 CRC64;

Query Match 39.9%; Score 960.5; DB 11; Length 387;
 Best Local Similarity 48.3%; Pred. No. 2.7e-86;
 Matches 171; Conservative 56; Mismatches 122; Indels 5; Gaps 4;

Qy	71	APPLSAPNYPTISRPLICRFGYQMDESNQCDVDECATDSHQCNPQTQICINTEGGYTCSC	130
		: : : : : : :	
Db	38	ADPQRIPSNP--SHRIQCAAGYEQSEHNVCQDIDECTSGTHNCRTDQVCINLRGSFTQC	95
Qy	131	TDGYWLLEGQCLDIDECRY-GYCQQLCANVPGSYSCTCNPGFTLNEDGRSCQDVNECATE	189
		: : : :	
Db	96	LPGYQKRGEQCVDIDECTVPPYCHQRCVNTPGSFYCQCSPGFQLAANNYTCVDINECDAS	155
Qy	190	NPCVQTCVNTYGSFICRCDPGYELEEDGVHCSDMDECSFSEFLCQHECVNQPPTYFCSCP	249
		: : : : :	
Db	156	NQCAQQCYNILGSFICQCNQGYELSSDRLNCEDIDECRTSSYLCQYQCVNEPGKFSCMCP	215
Qy	250	PGYILLDDNRSCQDINECEHRNHTCNLQQTTCYNLQGGFKCIDPIRCEEPYLRISDNRCMC	309
		: : : : : : :	
Db	216	QGYEVV-RSRTCQDINECETTNE-CREDEMWNHGGFRCYPRNPCQDHYVLTSENRCVC	273
Qy	310	PAENPGCRDQPFTILYRDMDVVSGRSVPADIFQMQATTRYPGAYYIFQIKSGNEGREFYM	369
		: : : : : :	
Db	274	PVSNTMCRELPQSIVYKYSIRSRSVPSDIFQIQATMIYANTINTFRIKSGNENGEFYL	333
Qy	370	RQTGPISATLVMTRPIKGPRIQLDLEMITVNTVINFRGSSVIRLRIYVSQYPF	423
		: : : : : : :	
Db	334	RQTSPVSAMLVLVKSLSGPREYIVDLEMLTVSSIGTFRTSSVLRLTIIVGPFPSF	387

RESULT 6

Q922K8

ID Q922K8 PRELIMINARY; PRT; 685 AA.
 AC Q922K8;
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE Similar to fibulin 1.
 GN FBLN1.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Strausberg R.;
 RL Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Urinary bladder;
 RX MEDLINE=22354683; PubMed=12466851;
 RA The FANTOM Consortium,
 RA the RIKEN Genome Exploration Research Group Phase I & II Team;
 RT "Analysis of the mouse transcriptome based on functional annotation of
 RT 60,770 full-length cDNAs.";
 RL Nature 420:563-573 (2002).
 DR EMBL; BC007140; AAH07140.1; -.
 DR EMBL; AK035388; BAC29054.1; -.
 DR MGD; MGI:95487; Fbln1.
 DR InterPro; IPR000020; Anaphylatoxin.
 DR InterPro; IPR000152; Asx_hydroxyl.
 DR InterPro; IPR001881; EGF_Ca.
 DR InterPro; IPR006209; EGF_like.
 DR Pfam; PF01821; ANATO; 3.
 DR Pfam; PF00008; EGF; 6.
 DR SMART; SM00104; ANATO; 3.
 DR SMART; SM00179; EGF_CA; 8.
 DR PROSITE; PS01177; ANAPHYLATOXIN_1; 3.
 DR PROSITE; PS01178; ANAPHYLATOXIN_2; 3.
 DR PROSITE; PS00010; ASX_HYDROXYL; 4.
 DR PROSITE; PS01186; EGF_2; 3.
 DR PROSITE; PS01187; EGF_CA; 8.
 KW EGF-like domain.
 SQ SEQUENCE 685 AA; 75283 MW; EF0D77D7F66B73B8 CRC64;

Query Match 30.8%; Score 741.5; DB 11; Length 685;
 Best Local Similarity 36.5%; Pred. No. 2.1e-64;
 Matches 158; Conservative 64; Mismatches 152; Indels 59; Gaps 16;

Qy	1	QCTNGFDLDRQSGQCLDIDECRTIPEACRGDMMCVNQNGGYLCIPRTNPVYRGYPYNSPYS	60
		: : :	
Db	295	QCKSGFIQD-ALGNCIDINECLSISAPCPVGQTCINTEGSYTC-----	336
Qy	61	TPYSGPYPAAPPLSAPNYPTISRPLICRFGYQM-DESNQCVDVDECATDSHCNPTQIC	119
		: :	
Db	337	-----QKNVPN-----CGRGYHLNEEGTRCVDVDECSPPAEPCGKGHHC	375
Qy	120	INTEGGYTCSCTDGYWL--LEGQCLDIDEC-RY--GYCQQLCANVPGSYSCTCNPGFTLN	174
		: : : : : : :	
Db	376	LNSPGSFRCCKAGFYFDGISRTCVDINECQRYPGRLCGHKCENTPGSFHCSCSAGFRLS	435
Qy	175	EDGRSCQDVNECATENPCVQTCVNTYGSFICRCDPGYELEE-DGVHCSDMDECSF--SEF	231
		: : :	
Db	436	VDGRSCEDVNEC-LNSPCSQECANVYGSYQCYCRRGYQLSDVDGVTCEDIDECALPTGGH	494
Qy	232	LCQHECVNQPGTYFCSCP-PGYILLDDNRSCQDINECEHRNHTCNLQQTTCYNLQGGFKCI	290
		: : : : : : : :	
Db	495	ICSYRCINIPGSFQCSCPSSGYRLAPNGRNCQDIDECVTGIHNCSINETCFNIQGSFRCL	554

Qy 232 LCQHECVNQPGTYFCSCP-PGYILLDDNRSCQDINECEHRNHTCNLQQTCYNLQGGFKCI 290
 :| : |:| ||:: ||| | | : |:| |||:| | |:: |:| |:| |:| |:| :|:
 Db 495 ICSYRCINIPGSFQCSCPSSGYRLAPNGRNCQDIDECVTGIHNCSINETCFNIQGSFRCL 554
 Qy 291 DPIRCEEPYLRISDNRC-MCPA-ENPGCRDQPFTILYRDMDVVSGRSVPADIFQMQATTR 348
 | | | | :| | | | | | | | : : | | | |:| :| :|
 Db 555 S-FECPENYRRSADTRCERLPCHENQECPRPLRITYYHLSFPTNIQVPAVVFRMGPSA 613
 Qy 349 YPGAYYIFQIKSGNEGREFYMRQTGPISATLVMTRPIKGPRIQLDLEM--ITVNTVIN 406
 || | :|| | | : | : |:| | |:: | :| | :| :| :|
 Db 614 VPGDSMQLAITAGNEEGFFTTRKVVSHHSGVVALTKPIPEPRDLLLTVKMDLYRHGTVSSF 673
 Qy 407 RGSSVIRLRIYVS 419
 | :| |:|
 Db 674 ----VAKLFIFVS 682

RESULT 8

Q8TBH8

ID Q8TBH8 PRELIMINARY; PRT; 683 AA.
 AC Q8TBH8;
 DT 01-JUN-2002 (TrEMBLrel. 21, Created)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE Fibulin 1.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RA Strausberg R.;
 RL Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; BC022497; AAH22497.1; -.
 DR InterPro; IPR000020; Anaphylatoxin.
 DR InterPro; IPR000152; Asx_hydroxyl.
 DR InterPro; IPR001881; EGF_Ca.
 DR InterPro; IPR006209; EGF_like.
 DR Pfam; PF01821; ANATO; 3.
 DR Pfam; PF00008; EGF; 6.
 DR SMART; SM00104; ANATO; 3.
 DR SMART; SM00179; EGF_CA; 8.
 DR PROSITE; PS01177; ANAPHYLATOXIN_1; 3.
 DR PROSITE; PS01178; ANAPHYLATOXIN_2; 3.
 DR PROSITE; PS00010; ASX_HYDROXYL; 4.
 DR PROSITE; PS01186; EGF_2; 3.
 DR PROSITE; PS01187; EGF_CA; 8.
 KW EGF-like domain.
 SQ SEQUENCE 683 AA; 74423 MW; 2665A3961B6403B4 CRC64;
 Query Match 30.6%; Score 735.5; DB 4; Length 683;
 Best Local Similarity 35.7%; Pred. No. 8.1e-64;
 Matches 155; Conservative 66; Mismatches 152; Indels 61; Gaps 16;

Qy 1 QCTNGFDLDRQSGQCLDIDECRTIPEACRGDMMCVNQNGGYLCIPRTNPVYRGFYSNPYS 60
 || :|| | | |:| |:| :| | | :| | |

Db 293 QCKSGFIQD-ALGNCIDINECLSISAPCPIGHTCINTEGSYTC----- 334

Qy 61 TPYSGPYPAAPPLSAPNYPTISRPLICRFGYQM-DESNQCVDVDECATDSHCNPTQIC 119
: || | || : : | : ||||| : | |

Db 335 -----QKNVPN-----CGRGYHLNEEGTRCVDVDECAPPAEPCGKGHRC 373

Qy 120 INTEGGYTCSTDGYWL--LEGQCLDIDEC-RY--GYCQQLCANVPGSYSCTCNPGFTLN 174
: | : | | || : : | : ||| | | | | : | : | | |

Db 374 VNSPGSFRCECKTGYYFDGISRMCDVNECQRYPGRLCGHKCENTLGSYLCSCSVGFRLS 433

Qy 175 EDGRSCQDVNECATENPCVQTCVNTYGSFICRCDPGYELEE-DGVHCSDMDECSF--SEF 231
| | | | : | : | : : | | | | | | : | | | : | | | | : | | |

Db 434 VDGRSCEDINECSS-SPCSQECANVYGSYQCYCRRGYQLSDVDGVTCEDIDECALPTGGH 492

Qy 232 LCQHECVNQPGTYFCSCP-PGYILLDDNRSCQDINECEHRNHTCNLQOTCYNLQGGFKCI 290
: | : | : | | | : | | | : : | | | : | | : | : | : | : | : |

Db 493 ICSYRCINIPGSFQCSCPSSGYRLAPNGSNCQDIDECVTGIHNCSINETCFNIQGGFRCL 552

Qy 291 DPIRCEEPYLRISDNRC-MCPA-ENPGCRDQPFTILYRMDVVSGRSVPADIFQMQATTR 348
| | | | : | | | | | | | | : : | | : | : | : |

Db 553 -AFECPENYRRSAATRCERLPCHENRECSKLPLRITYYHLSFPTNIQAPAVVFRMGPSA 611

Qy 349 YPGAYYIFQIKSGNEGREFYMRQTGPISATLVMTRPIKGPREIQLDLEMITVNTVINFRG 408
| | | | | | | | : | | : : | : | | : : : | : | : |

Db 612 VPGDSMQLAITGGNEEGFFTTRKVSPhSGVVALTKPVPEPRDL-----LLTVKMDLSRHG 666

Qy 409 ---SSVIRLRIYVS 419
| | : | | |

Db 667 TVSSFVAKLFIFVS 680

RESULT 9

Q99K58

ID Q99K58 PRELIMINARY; PRT; 1174 AA.

AC Q99K58;

DT 01-JUN-2001 (TrEMBLrel. 17, Created)

DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)

DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)

DE Similar to fibulin 2.

GN FBLN2.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI_TaxID=10090;

RN [1]

RP SEQUENCE FROM N.A.

RA Strausberg R.;

RL Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases.

DR EMBL; BC005443; AAH05443.1; -.

DR HSSP; P00736; 1APQ.

DR MGD; MGI:95488; Fbln2.

DR InterPro; IPR000020; Anaphylatoxin.

DR InterPro; IPR000152; Asx_hydroxyl.

DR InterPro; IPR001881; EGF_Ca.

DR InterPro; IPR006209; EGF_like.

DR Pfam; PF01821; ANATO; 2.

DR Pfam; PF00008; EGF; 6.

RP SEQUENCE FROM N.A.
 RA Brooke J.S., Cha J.-H., Eidels L.;
 RT "Cloning of monkey fibulin-1c gene."
 RL Submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; AF395659; AAM90567.1; -.
 DR InterPro; IPR000020; Anaphylatoxin.
 DR InterPro; IPR000152; Asx_hydroxyl.
 DR InterPro; IPR001881; EGF_Ca.
 DR InterPro; IPR006209; EGF_like.
 DR InterPro; IPR006210; IEGF.
 DR Pfam; PF01821; ANATO; 1.
 DR Pfam; PF00008; EGF; 3.
 DR SMART; SM00104; ANATO; 1.
 DR SMART; SM00181; EGF; 9.
 DR SMART; SM00179; EGF_CA; 9.
 DR PROSITE; PS01177; ANAPHYLATOXIN_1; 1.
 DR PROSITE; PS01178; ANAPHYLATOXIN_2; 1.
 DR PROSITE; PS00010; ASX_HYDROXYL; 4.
 DR PROSITE; PS01186; EGF_2; 3.
 DR PROSITE; PS01187; EGF_CA; 7.
 FT NON_TER 1 1
 SQ SEQUENCE 598 AA; 65516 MW; 849BF018DF452B02 CRC64;

Query Match 30.0%; Score 721; DB 6; Length 598;
 Best Local Similarity 35.3%; Pred. No. 1.9e-62;
 Matches 155; Conservative 72; Mismatches 184; Indels 28; Gaps 15;

Qy	2	CTNGFDLDRQSGQCLDIDECRTIPEACRGDMMCVNQNGGYLCIPR---TNPVYRGYPYNSP	58
		: : : : : : : : : : :	
Db	164	CGTGYEL-TEDNSCKDIDQCESGIHNCLPDFICQNTLGSFRCRPKLQCKNGFIQDALANC	222
Qy	59	YS-----TPYSGPYPAAPPLSAPNYPTISRPLICRFGYQMDESNQCVDVDECATDSHQ	113
		: : : : : : : : : :	
Db	223	IDINECLSIVSAPCPTGHTCINTEGSYQKNVPNCGRGYHLNEEGTRCDVNECAPPAEPC	282
Qy	114	NPTQICINTEGGYTCSCTDGYWL--LEGQCLDIDEC-RY--GYCQQLCANVPGSYSCTCN	168
		: : : : : : : : : : : :	
Db	283	GKGHRCVNSPGSFRCECKTGYIFYDGISRMCVDVNECQRYPGRLCGHKCENTLGSYVCS	342
Qy	169	PGFTLNEDGRSCQDVNECATENPCVQTCVNTYGSFICRCDPGYELEE-DGVHCSDMDECS	227
		: : : : : : : : : : :	
Db	343	VGFRLSVDGRSCEDINECSS-SPCSQECANVYGSYQCYCRRGYQLSDVDGVTCEIDICA	401
Qy	228	F--SEFLCQHECVNQPGTYFCSCP-PGYILLDDNRSCQDINECEHRNHTCNLQQTCYNLQ	284
		: : : : : : : : : : : :	
Db	402	LPTGGHICSYRCINIPGSFQCSCPASGYRLAPNGRNCQDIDECVTGIHNCSINETCFNIQ	461
Qy	285	GGFKCIDPIRCEEPYLRISDNRC-MCPA-ENPGCRDQPFTILYRDMDVVSGRSVPADIFQ	342
		: : : : : : : : : : : :	
Db	462	GGFRCL-AFECPENYRRSAATRCERLPCHENRECSKPLRITYYHLSFPTNIQAPAVVFR	520
Qy	343	MQATTRYPGAYYIFQIKSGNEGREFYMRQTGPISATLVMTRPIKGPRIQLDLEM--ITV	400
		: : : : : : : : : :	
Db	521	MGPSSAVPGDSMQLAITGGNEEGFFTTRKVSHPHSGVVALTKPVPEPRDLLLTVMKMDLYRH	580
Qy	401	NTVINFRGSSVIRLRIYVS	419
		: : :	

Db 581 GTVSSF----VAKLFIFVS 595

RESULT 11

O73774

ID O73774 PRELIMINARY; PRT; 704 AA.
AC O73774;
DT 01-AUG-1998 (TrEMBLrel. 07, Created)
DT 01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Fibulin-1, isoform D.
GN FBLN1.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99120531; PubMed=9923656;
RA Barth J.L., Argraves K.M., Roark E.F., Little C.D., Argraves W.S.;
RT "Identification of chicken and C. elegans fibulin-1 homologs and
RT characterization of the C. elegans fibulin-1 gene.";
RL Matrix Biol. 17:635-646(1998).
DR EMBL; AF051399; AAC05387.1; -.
DR HSSP; P00742; 1HCG.
DR InterPro; IPR000020; Anaphylatoxin.
DR InterPro; IPR000152; Asx_hydroxyl.
DR InterPro; IPR001881; EGF_Ca.
DR InterPro; IPR006209; EGF_like.
DR Pfam; PF01821; ANATO; 2.
DR Pfam; PF00008; EGF; 6.
DR SMART; SM00104; ANATO; 3.
DR SMART; SM00179; EGF_CA; 8.
DR PROSITE; PS01177; ANAPHYLATOXIN_1; 1.
DR PROSITE; PS01178; ANAPHYLATOXIN_2; 2.
DR PROSITE; PS00010; ASX_HYDROXYL; 5.
DR PROSITE; PS01186; EGF_2; 3.
DR PROSITE; PS01187; EGF_CA; 8.
KW EGF-like domain.
SQ SEQUENCE 704 AA; 78137 MW; D47D5A30D5E42932 CRC64;

Query Match 29.6%; Score 713; DB 13; Length 704;
Best Local Similarity 35.1%; Pred. No. 1.4e-61;
Matches 160; Conservative 64; Mismatches 154; Indels 78; Gaps 21;

QY 1 QCTNGFDLDRQSGQCLDIDECRTIPEACRGDMMCVNQNGGYLCIPRTNPVYRGYPYNSNPYS 60
|| ||| | | :|:|:| : | :|:| :| | | :|
Db 294 QCMNGFIQD-ALGNCIDINECLSTNMPCPAGQICINTDGSYTC-QRISP----- 340
QY 61 TPYSGPYPAAPPLSAPNYPTISRPLICRFGYQMD-SNQCVDVDECATDSHQCNPTQIC 119
| || :| :| ||||| :| | :|
Db 341 -----SCGRGYHLNEDGTRCVDVDECSSDQPCGEGHVC 374
QY 120 INTEGgyTCSCTDGYW--LLEGQCLDIDECRY---GYCQQLCANVPGSYSCNPGFTLN 174
|| | | | | || :| :|:|:| | | | | | | | | :|
Db 375 INGPgNYRCECKSGYSFDVISRTCIDINECRYPGRLLCAHKCENTPGSYyCTCTMGFKLS 434

Qy 175 EDGRSCQDVNECATENPCVQTCVNTYGSFICRCDPGYELEE-DGVHCSDMDECSF--SEF 231
 |||||:|:|:| : :|| | | | ||: | | :|:| : ||: | |:|:|:
 Db 435 SDGRSCEDLNECES-SPCSQECANVYGSYQCYCRRGFQLSDIDGISCEDIDECALPTGGH 493

Qy 232 LCQHECVNQPGTYFCSCP-PGYILLDDNRSCQDINECEHRNHTCNLQQTCYNLQGGFKCI 290
 :| :| ||:| :|| | | : :|:|:|:| | :| :|:|:|:|:|:|:
 Db 494 ICSFRCINIPGSFQCTCPSTGYRLAPNARNCQDIDECVAETHNCSFNETCFNIQGGFRCL 553

Qy 291 DPIRCEEPYLRISDN-----RCM--CPAENPGC-RDQPFTILYRDMDVVSGRSV-- 336
 : | | | : | ||: | : | | | : : : |
 Db 554 S-LECPENYRKSGDTRLEKTDITIRCIKSCRPNVDVNCVLDPVHTISHTVISLPTFRETR 612

Qy 337 PADIFQMQA-TTRYPG--AYYIFQIKSGNEGREF-----YMRQTGPISATLVMTRPIKGP 388
 | :| :|:| | || | || | || | || | : |||||
 Db 613 PEEIIFLRAITPTYPANQADIIFDITEGNLRESFDIIKRYM--DGMTVGVRQVRPIVGP 670

Qy 389 REIQLDLEM-ITVNTVINFRGSSVIRLRIYVSQYPF 423
 | ||| : |:| : : : |:|:| |
 Db 671 FHAILKLEMNYVMGGVVSRR--NIVNVHIFVSEYWF 704

RESULT 12

Q9Y3V7

ID Q9Y3V7 PRELIMINARY; PRT; 576 AA.
 AC Q9Y3V7;
 DT 01-NOV-1999 (TrEMBLrel. 12, Created)
 DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE Hypothetical protein (Fragment).
 GN DKFZP586A1519.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Uterus;
 RA Wambutt R., Heubner D., Mewes H.W., Gassenhuber J., Wiemann S.;
 RL Submitted (MAR-1999) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; AL050095; CAB43267.1; -.
 DR HSSP; P00736; 1APQ.
 DR InterPro; IPR000152; Asx_hydroxyl.
 DR InterPro; IPR001881; EGF_Ca.
 DR InterPro; IPR006209; EGF_like.
 DR Pfam; PF00008; EGF; 6.
 DR SMART; SM00179; EGF_CA; 8.
 DR PROSITE; PS00010; ASX_HYDROXYL; 4.
 DR PROSITE; PS01186; EGF_2; 4.
 DR PROSITE; PS01187; EGF_CA; 9.
 KW Hypothetical protein; EGF-like domain.
 FT NON_TER 1 1
 SQ SEQUENCE 576 AA; 63274 MW; FF2F0E9B185D8AC3 CRC64;

Query Match 29.2%; Score 703.5; DB 4; Length 576;
 Best Local Similarity 34.5%; Pred. No. 9.5e-61;
 Matches 142; Conservative 58; Mismatches 152; Indels 59; Gaps 11;

Query Match 29.2%; Score 702.5; DB 4; Length 1231;
Best Local Similarity 34.5%; Pred. No. 2.9e-60;
Matches 142; Conservative 58; Mismatches 152; Indels 59; Gaps 11;

Qy	1	QCTNGFDLDRQSGQCLDIDECRTIPEACRGDMMCVNQGYYGLCIPRTNPVYRGFPYSNPYS	60
		: : : : : : : : : :	
Db	842	RCMDGF-LQDPEGNCVDINECTSLSEPCRPGFSCINTVGSYTC-----	883
Qy	61	TPYSGPYPAAPPLSAPNYPTISRPLICRFGYQ-MDESNQCVDVDECATDSHQCNPTQIC	119
		: : : : :	
Db	884	-----QRNPLICARGYHASDDGXKCVDVNECETGVHRCGEGQVC	922
Qy	120	INTEGGYTCSTDGYW--LLEGQCLDIDECRYG---YCQQLCANVPGSYSCTCNPGFTLN	174
		: : :	
Db	923	HNLPGSYRCDCKAGFQRDAFGRGCIDVNECWASPGRLCQHTCENTLGSYRCSASCASGFLLA	982
Qy	175	EDGRSCQDVNECATENPCVQTCVNTYGSFICRCDPGYELEEDGVHCSMDDECS-FSEFLC	233
		: : : : : :	
Db	983	ADGKRCEQDVNECEAQR-CSQECANIYGSYQCYCRQGYQLAEDGHTCTDIDECAQGAGILC	1041
Qy	234	QHECVNQPGTYFCSCP-PGYILLDDNRSCQDINECEHRNHTCNLQQTTCYNLQGGFKCIDP	292
		: : : : : : : : :	
Db	1042	TFRCLNVPGSYQCACPEQGYTMTANGRSCKDVDECALGTHNCSEAETCHNIQGSFRCL-R	1100
Qy	293	IRCEEPYLRI SDNRCMCPAENPGCRD-----QPFTILYRDMDVVSGRSVPADIFQMQAT	346
		: : : : : : : :	
Db	1101	FECPPNYVQVSKTKC---ERTTCHDFLECQNSPARITHYQLNFQTGLLVPAHIFRIGPA	1156
Qy	347	TRYPGAYYIFQIKSGNEGREFYMRQTGPISATLVMTRPIKGPREIQLDLEM	397
		: : : : : : : :	
Db	1157	PAFTGDTIALNIIKGNEEGYFGTRRLNAYTGVVYLORAVLEPRDFALDVEM	1207

RESULT 14

Q8IUI0

ID Q8IUI0 PRELIMINARY; PRT: 1231 AA.

AC Q8IUI0;

DT 01-MAR-2003 (TrEMBLrel. 23, Created)

DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)

DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)

DE Fibulin 2.

GN FBLN2.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RA Li D., Marian A.J., Roberts R.;

RT "Identification of a novel alternatively spliced isoform of human

RT fibulin-2 gene abundantly expressed in heart and genetic evaluation in
RT patients with ARVD.":

RL (In) Unknown A. (eds.);

RL ABSTRACTS OF THE 52ND ANNUAL MEETING OF THE AMERICAN SOCIETY OF HUMAN

RL GENETICS, pp.323-323, Unknown Publisher (2002).

DR EMBL; AY130459; AAN05436.1; -.

SQ SEQUENCE 1231 AA; 131790 MW; 95D69EB2082952A7 CRC64:

Query Match 29.1%; Score 701.5; DB 4; Length 1231;
 Best Local Similarity 34.5%; Pred. No. 3.6e-60;
 Matches 142; Conservative 58; Mismatches 152; Indels 59; Gaps 11;

```

Qy      1 QCTNGFDLDRQSGQCLDIDECRTIPEACRGDMMCVNQNGGYLCIPRTNPVYRGYPYNSNPYS 60
      :| :|| | | :|:|:| :| :| | | :| | | |
Db      842 RCMDGF-LQDPEGNCVDINECTSLSEPCRPFGFSCINTVGSYTC----- 883

Qy      61 TPYSGPYPAAPPLSAPNYPTISRPLICRFGYQ-MDESNQCVDVDECATDSHCNPTQIC 119
      |||| | | :| :|||:| | | :| | :|
Db      884 -----QRNPLICARGYHASDDGAKCVDVNECETGVHRCGEGQVC 922

Qy     120 INTEGgyTCSTdgyw--LLEGQCLDIDECRYG--YCQQLCANVPGSYSCTCNPGFTLN 174
      | | | | | :| :|:|:| | | | | | | | | |
Db     923 HNLPgsYRCdCKAGfQRDAfGRGCI dVNECWASpGRlCQHTCENTlGSYRCSCASGfLLA 982

Qy     175 EDGRSCQDVNECATENPCVQTCVNTYGSFICRCDPGYELEEDGVHCSDMDECS-FSEFLC 233
      ||: |:| ||| :| | | | ||: | | ||: ||| |:| ||| :| |
Db     983 ADGKRCEdVNECEaQR-CSQECANIYGSYQCYCRQGYQLAEDGHTCTDIDeCAQGAGILC 1041

Qy     234 QHECVNQPGTYFCSCP-PGYILLDDNRSCQDINECEHRNHTCNLQQTcyNLQGGfKCIDP 292
      |:| ||:| |:| | | :| :| ||:|:| | | | :| |:| |:| |:| |:|
Db    1042 TFRCLNVPGSYQCACPEQGYTMTANGRSCKDVDECALGTHNCSEAETCHNIQGSFRCL-R 1100

Qy     293 IRCEEPYLRISDNRCMCPAENPGCRD-----QPFTILYRDMDVVSGRSVPADIFQMqAT 346
      | | |:| :| | | | | | | :| :| :| | | | |:|
Db    1101 FECPPNYVQVSKTKC----ERTTCHDFLEcQNSPARITHYQLNFQTGLLVPAHIFRIGPA 1156

Qy     347 TRYPGAYYIFQIKSGNEGREFYMRQTGPISATLVMTRPIKGPREIQLDLEM 397
      :| | | | | | :| :| :| :| :| | | | |:|
Db    1157 PAFTGDTIALNIiKGNEEGYfGTRRLNAYtGVVYLQRAVLEPRDFALDVEM 1207
  
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RESULT 15

Q8NBH6

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ID   Q8NBH6          PRELIMINARY;          PRT;          638 AA.
AC   Q8NBH6;
DT   01-OCT-2002 (TrEMBLrel. 22, Created)
DT   01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT   01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE   Hypothetical protein NT2RP3003649.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Ota T., Nishikawa T., Suzuki Y., Kawai-Hio Y., Hayashi K., Ishii S.,
RA   Saito K., Yamamoto J., Wakamatsu A., Nagai T., Nakamura Y.,
RA   Nagahari K., Sugano S., Isogai T.;
RT   "HRI human cDNA sequencing project.";
RL   Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AK075566; BAC11705.1; -.
DR   InterPro; IPR000020; Anaphylatoxin.
DR   InterPro; IPR000152; Asx_hydroxyl.
DR   InterPro; IPR001881; EGF_Ca.
  
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DR InterPro; IPR006209; EGF_like.
 DR InterPro; IPR006210; IEGF.
 DR Pfam; PF01821; ANATO; 1.
 DR Pfam; PF00008; EGF; 4.
 DR SMART; SM00181; EGF; 9.
 DR SMART; SM00179; EGF_CA; 9.
 DR PROSITE; PS00010; ASX_HYDROXYL; 4.
 DR PROSITE; PS01186; EGF_2; 3.
 DR PROSITE; PS01187; EGF_CA; 8.
 KW Hypothetical protein.
 SQ SEQUENCE 638 AA; 70577 MW; EBC0DE3147A7621F CRC64;

Query Match 28.9%; Score 695; DB 4; Length 638;
 Best Local Similarity 34.5%; Pred. No. 7.4e-60;
 Matches 159; Conservative 65; Mismatches 149; Indels 88; Gaps 21;

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Qy      1 QCTNGFDLDRQSGQCLDIDECRTIPEACRGDMMCVNQNGGYLCIPRTNPVYRGYPYNSNPYS 60
      || :|| | | :||:| | :| | | | | | |
Db      228 QCKSGFIQD-ALGNCIDINECLSISAPCPIGHTCINTEGSYTC----- 269

Qy      61 TPYSGPYPAAPPLSAPNYPTISRPLICRFGYQM-DESNQCVDVDECATDSHCNPTQIC 119
      : || | | : : | | | | | | : | |
Db      270 -----QKNVPN-----CGRGYHLNEEGTRCVDVDECAPPAEPCGKGHRC 308

Qy      120 INTEGGYTCSCTDGYWL--LEGQCLDIDEC-RY--GYCQQLCANVPGSYSCTCNPGFTLN 174
      :| : | | | | : | :|:| | | | | | | | | | | | :
Db      309 VNSPGSFRCECKTGYYFDGISRMCDVNECQRYPGRLCGHKCENTLGSYLCSCSVGFRLS 368

Qy      175 EDGRSCQDVNECATENPCVQTCVNTYGSFICRCDPGYELEE-DGVHCSDMDECSF--SEF 231
      |||||:|:|:|:|:|:| | | | | | | | | | | | | |
Db      369 VDGRSCEDINECSS-SPCSQECANVYGSYQCYCRRGYQLSDVDGVTCEDIDECALPTGGH 427

Qy      232 LCQHECVNQPGTYFCSCP-PGYILLDDNRSCQDINECEHRNHTCNLQOTCYNLQGGFKCI 290
      :| : | :| | | | | | | | : | :| | | | | | | | :
Db      428 ICSYRCINIPGSFQCSCPSSGYRLAPNGRNCQDIDECVTGIHNCSINETCFNIQGGFRCL 487

Qy      291 DPIRCEEPYLRISDN-----RCMCPAENPGCRDQPFTILYRDMDVVSGRSV----- 336
      | | | | : | | | | | | | | | | | | | | :
Db      488 -AFECPENYRRSAATLQQEKTDTVRCI-----KSCRPNVDVTCVFDVPVHTISHTVISLPTF 541

Qy      337 -----PADIFQMQA-TTRYPG--AYYIFQIKSGNEGREF-----YMRQTGPISATLVMTR 383
      | : | :| | :| | | | | | | | | | | | : |
Db      542 REFTRPEEIIIFLRAITPPHPASQANIIFDITEGNLRDSFDIIKRYM--DGMTVGVVVRQVR 599

Qy      384 PIKGPREIQLDLEM-ITVNTVINFRGSSVIRLRIYVSQYPF 423
      || || | || | | :| :| : | :| | | |
Db      600 PIVGPFHAVLKLEMNYVVGGVVSHR--NVNVNHIFVSEYWF 638

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Search completed: January 9, 2004, 12:36:57
 Job time : 33.5385 secs